

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Man-Tam DAVIS Examiner #: 13422 Date: 2/12/2003
 Art Unit: 1042 Phone Number 305-2008 Serial Number: 091403440
 Mail Box and Bldg/Room Location: 8E12 8A01 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

newly checked
04/97

Jan Delaval
Reference Librarian
Library & Chemical Library
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delaval@uspis.gov

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Searcher: Man-Tam DAVIS

Searcher Phone #: 305-2008

Searcher Location: _____

Date Searcher Picked Up: 2/12/03

Date Completed: 2/12/03

Searcher Prep & Review Time: _____

Clerical Prep Time: 70

Online Time: 70

Type of Search

NA Sequence (#) _____

AA Sequence (#) ✓

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel/Orbit _____

Dr.Link _____

Lexis/Nexis _____

Sequence Systems ✓

WWW/Internet _____

Other (specify) _____

the first of these is the fact that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The second is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The third is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The fourth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The fifth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The sixth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The seventh is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The eighth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The ninth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The tenth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The eleventh is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The twelfth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

The thirteenth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable. The fourteenth is that the system is not a simple one. It is a complex system, and the behavior of the system is not predictable.

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:42 ; Search time 17.4167 Seconds
(without alignments)
32.098 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDMLWKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilesl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	20	4	US-09-081-975-8
2	99	94.3	20	4	US-09-081-975-10
3	99	94.3	20	4	US-09-081-975-11
4	99	94.3	20	4	US-09-081-975-16
5	94	89.5	20	4	US-09-081-975-14
6	94	89.5	20	4	US-09-081-975-15
7	90	85.7	19	4	US-09-081-975-13
8	86	81.9	20	4	US-09-081-975-19
9	77	73.3	15	1	US-08-277-660A-1
10	77	73.3	15	1	US-08-277-660A-4
11	77	73.3	15	1	US-08-424-957-1
12	77	73.3	15	1	US-08-424-957-20
13	77	73.3	15	4	US-09-035-686-1
14	77	73.3	15	4	US-09-035-686-20
15	74	70.5	15	1	US-08-277-660A-5
16	74	70.5	15	1	US-08-424-957-21
17	74	70.5	15	4	US-09-035-686-21
18	74	70.5	16	4	US-09-081-975-23
19	74	70.5	20	4	US-09-081-975-20
20	72	68.6	20	4	US-09-081-975-18
21	65	61.9	15	3	US-09-280-047-6
22	65	61.9	15	4	US-08-208-573B-6
23	65	61.9	15	5	PCT-US95-02856-6
24	60	57.1	18	4	US-09-081-975-22
25	59	56.2	11	1	US-08-277-660A-9
26	59	56.2	11	1	US-08-424-957-17
27	59	56.2	11	4	US-09-035-686-17

28 59 56.2 13 4 US-09-236-415-5
29 57 54.3 11 1 US-08-424-957-45
30 57 54.3 11 1 US-08-424-957-46
31 57 54.3 11 4 US-09-035-686-45
32 57 54.3 11 4 US-09-035-686-46
33 57 54.3 14 4 US-09-400-653A-7
34 57 54.3 14 4 US-09-248-061B-7
35 56 53.3 11 1 US-08-277-660A-10
36 56 53.3 11 1 US-08-277-660A-15
37 56 53.3 11 1 US-08-424-957-23
38 56 53.3 11 1 US-08-424-957-28
39 56 53.3 11 1 US-08-424-957-40
40 56 53.3 11 4 US-09-035-686-23
41 56 53.3 11 4 US-09-035-686-28
42 56 53.3 11 4 US-09-035-686-40
43 55 52.4 10 1 US-08-277-660A-7
44 55 52.4 10 1 US-08-424-957-11
45 55 52.4 10 4 US-09-035-686-11

ALIGNMENTS

RESULT 1
US-09-081-975-8
; Sequence 8, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-975-8

Query Match 94.3%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 2

US-09-081-975-10
 ; Sequence 10, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; APPLICANT: Jost, Christine
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP
 ; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081.975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eisenstein, Ronald I
 ; REGISTRATION NUMBER: 30,628
 ; REFERENCE/DOCKET NUMBER: 47400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-6054
 ; TELEFAX: 617-345-1300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-081-975-10

Query Match 94.3%; Score 99; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 3

US-09-081-975-11
 ; Sequence 11, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; APPLICANT: Jost, Christine
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP

; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081.975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eisenstein, Ronald I
 ; REGISTRATION NUMBER: 30,628
 ; REFERENCE/DOCKET NUMBER: 47400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-6054
 ; TELEFAX: 617-345-1300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-081-975-11

Query Match 94.3%; Score 99; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 4

US-09-081-975-16
 ; Sequence 16, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; APPLICANT: Jost, Christine
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP
 ; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081.975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:

NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054
 TELEFAX: 617-345-1300
 TELEX:
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-081-975-16

Query Match 94.3%; Score 99; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5

US-09-081-975-14
 Sequence 14, Application US/09081975
 Patent No. 6451979
 GENERAL INFORMATION:
 APPLICANT: Kaelin, William
 APPLICANT: Jost, Christine
 TITLE OF INVENTION: METHODS OF TREATMENT USING
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/046,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054
 TELEFAX: 617-345-1300
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-081-975-14

Query Match 89.5%; Score 94; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 6

US-09-081-975-15
 Sequence 15, Application US/09081975
 Patent No. 6451979
 GENERAL INFORMATION:
 APPLICANT: Kaelin, William
 APPLICANT: Jost, Christine
 TITLE OF INVENTION: METHODS OF TREATMENT USING
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/046,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054
 TELEFAX: 617-345-1300
 TELEX:
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-081-975-15

Query Match 89.5%; Score 94; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 7

US-09-081-975-13
 Sequence 13, Application US/09081975
 Patent No. 6451979
 GENERAL INFORMATION:
 APPLICANT: Kaelin, William
 APPLICANT: Jost, Christine
 TITLE OF INVENTION: METHODS OF TREATMENT USING
 TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/046,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054
 TELEFAX: 617-345-1300
 TELEX:
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-081-975-13

Query Match 89.5%; Score 94; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-081-975-13
Query Match 85.7%; Score 90; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.2e-08;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLSQETFSDLWKLLPEN 18
DB 1 PPLSQETFSLWNLLEN 18
|||||:|||||
;
RESULT 8
US-09-081-975-19
; Sequence 19, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997

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; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-081-975-19
Query Match 81.9%; Score 86; DB 4; Length 20;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPEN 18
DB 3 PLSQETFSDLWKLLPPN 19
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RESULT 9
US-08-277-660A-1
; Sequence 1, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-277-660A-1
Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLPEN 18
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Db      1 QETFSDLWLKLPEN 14

RESULT 10
US-08-277-660A-4
; Sequence 4, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-1

Query Match      73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QETFSDLWLKLPEN 18
Db      1 QETFSDLWLKLPEN 14

RESULT 12
US-08-424-957-20
; Sequence 20, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 20:

Db      1 PPLSQETFSDLWKL 14
Db      2 PPLSQETFSDLWKL 15

RESULT 11
US-08-424-957-1
; Sequence 1, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-4

Query Match      73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PPLSQETFSDLWKL 14
Db      2 PPLSQETFSDLWKL 15
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SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-424-957-20

Query Match 73.3%; Score 77; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
 |||||
 Db 2 PPLSQETFSDLWKL 15

RESULT 13

US-09-035-686-1

; Sequence 1, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957
 ; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WH
 ; TELEPHONE: (415) 398-3249
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-09-035-686-1

Query Match 73.3%; Score 77; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLEN 18
 |||||
 Db 1 QETFSDLWKLLEN 14

RESULT 14

US-09-035-686-20
 ; Sequence 20, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957
 ; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WH
 ; TELEPHONE: (415) 398-3249
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-09-035-686-20

Query Match 73.3%; Score 77; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
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 Db 2 PPLSQETFSDLWKL 15

RESULT 15

US-08-277-660A-5

; Sequence 5, Application US/08277660A
 ; Patent No. 5702908
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; US-08-277-660A-5

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-5

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Query Match      70.5%; Score 74; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY  2 PLSQETFSDLWKLLP 16
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Db  1 PLSQETFSGLWKLLP 15

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Job time : 17.9167 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:14:12 ; Search time 26.9167 Seconds
(without alignments)
59.144 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 159213

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	87.6	19	7	US-60-438-805-9
2	81	77.1	15	6	US-10-211-088-141
3	70	66.7	13	5	US-09-701-080C-22
4	70	66.7	13	5	US-09-701-080C-27
5	59	56.2	11	5	US-09-189-702A-286
6	41	39.0	14	6	US-10-049-428-6
7	40	38.1	7	5	US-09-701-080C-12
8	35	33.3	14	6	US-10-049-428-7
9	31.5	30.0	14	6	US-10-268-332-53
10	31.5	30.0	16	6	US-10-225-567A-1177
11	31	29.5	9	5	US-09-189-702A-7
12	31	29.5	12	5	US-09-281-717A-31
13	31	29.5	12	5	US-09-281-717A-33
14	31	29.5	12	5	US-09-281-717A-35
15	31	29.5	12	5	US-09-830-693B-6
16	31	29.5	12	5	US-09-830-693B-8
17	31	29.5	22	6	US-10-203-138A-12722
18	31	29.5	24	6	US-10-212-499-23
19	30	28.6	16	6	US-10-348-131-49
20	30	28.6	22	6	US-10-283-599-28
21	30	28.6	22	6	US-10-263-162-61
22	29	27.6	15	6	US-10-169-026-3
23	29	27.6	16	6	US-10-225-567A-942
24	29	27.6	17	1	PCT-US02-28371-70
25	29	27.6	17	6	US-10-236-878-70
26	29	27.6	18	5	US-09-552-802B-30

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27 29 27.6 20 6 US-10-319-786-54 Sequence 54, Appl
28 29 27.6 21 6 US-10-190-866A-6 Sequence 6, Appli
29 29 27.6 22 6 US-10-283-599-149 Sequence 149, App
30 28.5 27.1 18 5 US-09-632-036E-11 Sequence 11, Appl
31 28.5 27.1 20 7 US-60-438-805-3 Sequence 3, Appli
32 28 26.7 7 6 US-10-174-717A-36 Sequence 36, Appl
33 28 26.7 16 7 US-60-427-045-297 Sequence 297, App
34 28 26.7 18 6 US-10-283-599-219 Sequence 219, App
35 28 26.7 18 6 US-10-232-410-9 Sequence 9, Appli
36 28 26.7 20 6 US-10-299-867-60 Sequence 60, Appl
37 28 26.7 22 6 US-10-203-138A-15194 Sequence 15194, A
38 27 25.7 9 5 US-09-641-528-25751 Sequence 25751, A
39 27 25.7 9 5 US-09-641-528-29042 Sequence 29042, A
40 27 25.7 9 5 US-09-641-528A-25751 Sequence 25751, A
41 27 25.7 9 5 US-09-641-528A-29042 Sequence 29042, A
42 27 25.7 9 6 US-10-029-206A-67 Sequence 67, Appl
43 27 25.7 9 6 US-10-301-644-18 Sequence 18, Appl
44 27 25.7 9 6 US-10-028-075B-67 Sequence 67, Appl
45 27 25.7 10 5 US-09-641-528-463 Sequence 463, App

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ALIGNMENTS

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RESULT 1
US-60-438-805-9
; Sequence 9, Application US/60438805
; GENERAL INFORMATION:
; APPLICANT: KODAREK, THOMAS
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS
; FILE REFERENCE: UTSD:935USPI
; CURRENT APPLICATION NUMBER: US/60/438,805
; CURRENT FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-60-438-805-9

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Query Match 87.6%; Score 92; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18
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Db 1 PLSQETFSDLWKLLPEN 17

RESULT 2
US-10-211-088-141
; Sequence 141, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT

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; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Binding domain
 US-10-211-088-141

Query Match 77.1%; Score 81; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKL 15
 |||||
 Db 1 PPLSQETFSDLWKL 15

RESULT 3

US-09-701-080C-22
 ; Sequence 22, Application US/09701080C
 ; GENERAL INFORMATION:
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
 ; FILE REFERENCE: N73477C GCW
 ; CURRENT APPLICATION NUMBER: US/09/701,080C
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR FILING DATE: 1998-05-26
 ; PRIOR APPLICATION NUMBER: GB 9811303.8
 ; PRIOR FILING DATE: 1998-05-26
 ; PRIOR APPLICATION NUMBER: GB 9900157.0
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
 US-09-701-080C-22

Query Match 66.7%; Score 70; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKL 16
 |||||
 Db 1 SQETFSDLWKL 13

RESULT 4

US-09-701-080C-27
 ; Sequence 27, Application US/09701080C
 ; GENERAL INFORMATION:
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
 ; FILE REFERENCE: N73477C GCW
 ; CURRENT APPLICATION NUMBER: US/09/701,080C
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR FILING DATE: 1998-05-26
 ; PRIOR APPLICATION NUMBER: GB 9900157.0
 ; PRIOR FILING DATE: 1999-01-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
 US-09-701-080C-27

Query Match 66.7%; Score 70; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKL 16
 |||||
 Db 1 SQETFSDLWKL 13

RESULT 5

US-09-189-702A-286
 ; Sequence 286, Application US/09189702A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Kast, W. Martin
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Epimmune, Inc.
 ; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
 ; FILE REFERENCE: 39963-20019.20
 ; CURRENT APPLICATION NUMBER: US/09/189,702A
 ; CURRENT FILING DATE: 1998-11-10
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 286
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p53.14 peptide 34.0324
 US-09-189-702A-286

Query Match 56.2%; Score 59; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LSQETFSDLWK 13
 |||||
 Db 1 LSQETFSDLWK 11

RESULT 6

US-10-049-428-6
 ; Sequence 6, Application US/10049428
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles, Ian G.
 ; APPLICANT: Xu, Weiming
 ; APPLICANT: Liu, Lizhi
 ; TITLE OF INVENTION: Unducible Screen for Drug Discovery
 ; FILE REFERENCE: HO-P02380USO
 ; CURRENT APPLICATION NUMBER: US/10/049,428
 ; CURRENT FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: GB 9918077
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: GB 0016171.1
 ; PRIOR FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: HUMAN
 US-10-049-428-6

Query Match 39.0%; Score 41; DB 6; Length 14;
 Best Local Similarity 69.2%; Pred. No. 4.3;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWK 13
 |||||
 Db 2 PPLSQEAFALLKK 14

RESULT 7
US-09-701-080C-12
; Sequence 12, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 P
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-12

Query Match 38.1%; Score 40; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FSDLWKL 14
| | | | |
Db 1 FSDLWKL 7

RESULT 8
US-10-049-428-7
; Sequence 7, Application US/10049428
; GENERAL INFORMATION:
; APPLICANT: Charles, Ian G.
; APPLICANT: Xu, Weiming
; APPLICANT: Liu, Lishi
; TITLE OF INVENTION: Unducible Screen for Drug Discovery
; FILE REFERENCE: HO-P02380US0
; CURRENT APPLICATION NUMBER: US/10/049,428
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: GB 9918077
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: GB 0016171.1
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutagen
US-10-049-428-7

Query Match 33.3%; Score 35; DB 6; Length 14;
Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

Qy 1 PPLSQETFSDLWK 13
| | | | |
Db 2 PPLSEQAFALLKK 14

RESULT 9
US-10-268-332-53
; Sequence 53, Application US/10268332
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY3, EXPRESSED HIGHLY

; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-53

Query Match 30.0%; Score 31.5; DB 6; Length 14;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 6 BTFSDELWK 13
| | | | |
Db 5 ESFSDWLWK 13

RESULT 10
US-10-225-567A-1177
; Sequence 1177, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1177
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1177

Query Match 30.0%; Score 31.5; DB 6; Length 16;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 4 SQETFSDLWKLLPEN 18
| | | | |
Db 5 SQENHS---RLPEN 16

RESULT 11
US-09-189-702A-7
; Sequence 7, Application US/09189702A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Kast, W. Martin
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune, Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 39963-20019.20

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; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.24V9 peptide 1323.02
US-09-189-702A-7

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Query Match      29.5%; Score 31; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 13 KLLPEN 18
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Db 1 KLLPEN 6

```

```

RESULT 12
US-09-281-717A-31
; Sequence 31, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (5)..(5)
; OTHER INFORMATION: Leu --> Arg (L454R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)..(7)
; OTHER INFORMATION: Leu --> Arg (L456R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)..(8)
; OTHER INFORMATION: Glu --> Lys (E457K)
US-09-281-717A-31

```

```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 PPLSQETFS 10
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Db 3 PPLFLEVPED 12

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RESULT 13
US-09-281-717A-33

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; Sequence 33, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-33

```

```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFS 10
   |||
Db 3 PPLFLEVPED 12

```

```

RESULT 14
US-09-281-717A-35
; Sequence 35, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-35

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```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFS 10
   |||
Db 3 PPLFLEVPED 12

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```

RESULT 15
US-09-830-693B-6
; Sequence 6, Application US/09830693B

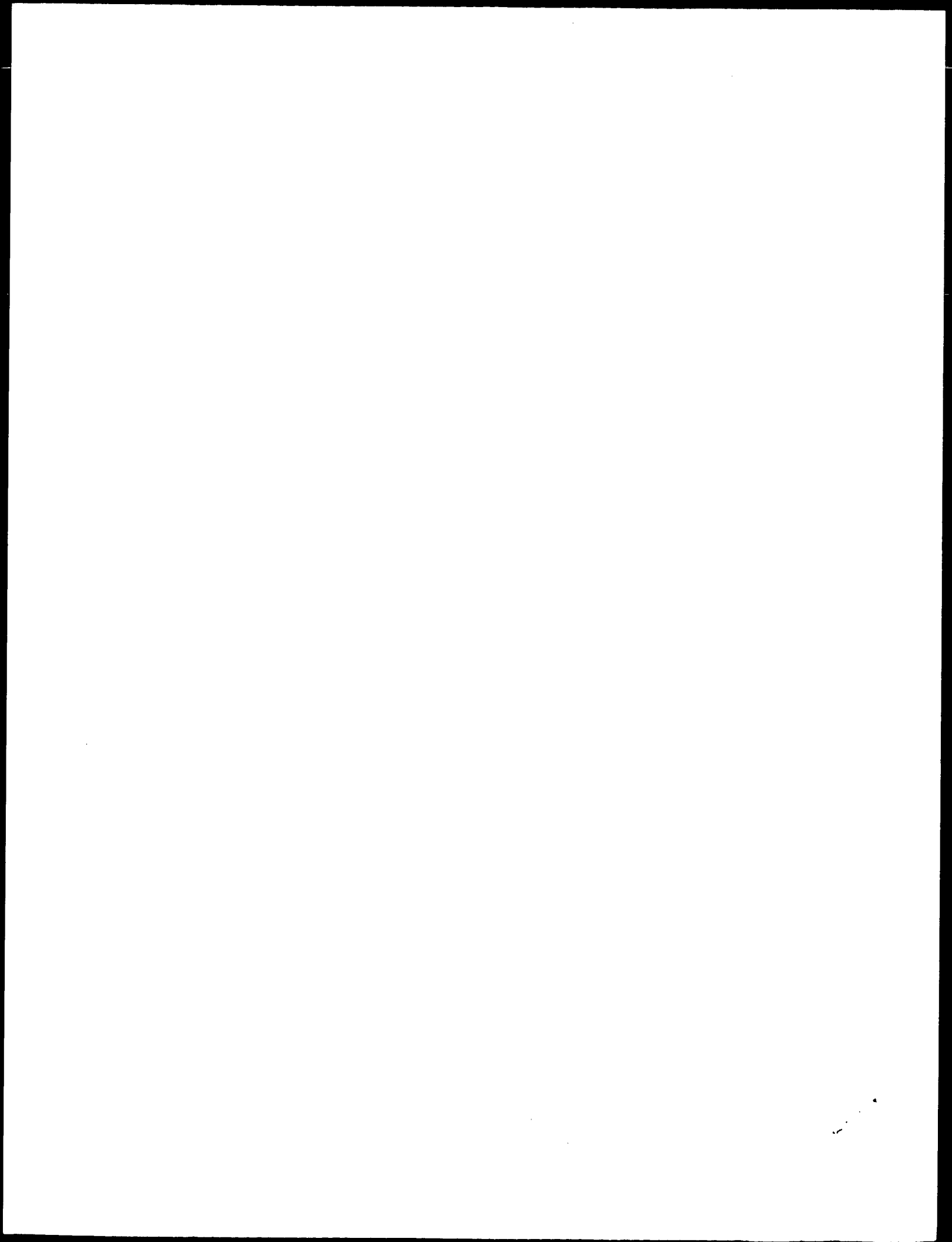
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; GENERAL INFORMATION:
; APPLICANT: Shiau, Andrew
; APPLICANT: Kushner, Peter
; APPLICANT: Agard, David
; APPLICANT: Greene, Geoffrey
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 9811-013-999
; CURRENT APPLICATION NUMBER: US/09/830,693B
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/06937
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US 60/113,014
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-693B-6
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Query Match          29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 PPLSQFTSD 10
   |||
Db 3 PPLFLEVFED 12
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Search completed: February 12, 2003, 11:24:44
Job time : 26.9167 secs
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:13:52 ; Search time 377.625 Seconds
(without alignments)
32.439 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 2260083

Minimum DB seq length: 0
Maximum Match length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:

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15: /cgn2_6/ptodata/1/paa/US091_COMB.pcp.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pcp.*
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27: /cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	US-09-403-440A-2	Sequence 2, Appli
2	99	94.3	18	US-09-214-371-74	Sequence 74, Appli
3	99	94.3	20	US-10-155-059-8	Sequence 8, Appli
4	99	94.3	20	US-10-155-059-10	Sequence 10, Appli
5	99	94.3	20	US-10-155-059-11	Sequence 11, Appli
6	99	94.3	20	US-10-155-059-16	Sequence 16, Appli

7	99	94.3	25	6	US-08-244-476-18	Sequence 18, Appli
8	99	94.3	25	8	US-08-424-273-1	Sequence 1, Appli
9	94	89.5	20	25	US-10-155-059-14	Sequence 14, Appli
10	94	89.5	20	25	US-10-155-059-15	Sequence 15, Appli
11	93	88.6	22	16	US-09-214-371-73	Sequence 73, Appli
12	92	87.6	19	21	US-09-732-384-7	Sequence 7, Appli
13	90	85.7	19	25	US-10-155-059-13	Sequence 13, Appli
14	89	84.8	19	16	US-09-214-371-1	Sequence 1, Appli
15	86	81.9	20	25	US-10-155-059-19	Sequence 19, Appli
16	77	73.3	15	6	US-08-277-660-1	Sequence 1, Appli
17	77	73.3	15	6	US-08-277-660-4	Sequence 1, Appli
18	77	73.3	15	8	US-08-424-273-3	Sequence 3, Appli
19	77	73.3	15	8	US-08-424-273-4	Sequence 4, Appli
20	77	73.3	15	18	US-09-458-297-1109	Sequence 1109, Ap
21	77	73.3	15	18	US-09-458-297-1469	Sequence 1469, Ap
22	77	73.3	15	18	US-09-458-297A-1109	Sequence 1109, Ap
23	77	73.3	15	18	US-09-458-297A-1469	Sequence 1469, Ap
24	77	73.3	15	21	US-09-732-384-6	Sequence 6, Appli
25	77	73.3	15	23	US-09-936-956-2	Sequence 2, Appli
26	77	73.3	15	23	US-09-936-956-3	Sequence 3, Appli
27	77	73.3	15	23	US-09-936-956-4	Sequence 4, Appli
28	77	73.3	17	16	US-09-265-927-3	Sequence 3, Appli
29	77	73.3	25	27	US-60-397-136-2	Sequence 2, Appli
30	74	70.5	15	6	US-08-277-660-5	Sequence 5, Appli
31	74	70.5	15	23	US-09-936-956-5	Sequence 5, Appli
32	74	70.5	15	23	US-09-936-956-9	Sequence 9, Appli
33	74	70.5	16	25	US-10-155-059-23	Sequence 23, Appli
34	74	70.5	18	20	US-09-695-437A-63	Sequence 63, Appli
35	74	70.5	20	25	US-10-155-059-20	Sequence 20, Appli
36	73	69.5	15	5	US-08-132-284-8	Sequence 8, Appli
37	73	69.5	15	7	US-08-398-139B-8	Sequence 8, Appli
38	73	69.5	15	20	US-09-695-437A-8	Sequence 8, Appli
39	73	69.5	15	23	US-09-936-956-13	Sequence 13, Appli
40	73	69.5	24	5	US-08-132-284-26	Sequence 26, Appli
41	73	69.5	25	5	US-08-132-284-4	Sequence 4, Appli
42	73	69.5	25	7	US-08-398-139B-4	Sequence 4, Appli
43	73	69.5	25	20	US-09-695-437A-4	Sequence 4, Appli
44	72	68.6	20	25	US-10-155-059-18	Sequence 18, Appli
45	71	67.6	15	23	US-09-936-956-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-403-440A-2
; Sequence 2, Application US/09403440A
; GENERAL INFORMATION:
; APPLICANT: Lane, David Philip
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
; TITLE OF INVENTION: INHIBITING THE INTERACTION OF P53 AND MDM2
; FILE REFERENCE: MEMB25.001APC
; CURRENT APPLICATION NUMBER: US/09/403,440A
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: PCT/GB98/01144
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: GB 9708092.3
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-403-440A-2

Query Match 100.0%; Score 105; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPENG 19
Db 1 PPLSQETFSDLWKLLPENG 19

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RESULT 2
US-09-214-371-74
; Sequence 74, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickel, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Scheverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match          94.3%; Score 99; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 3
US-10-155-059-8
; Sequence 8, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTI-BODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; INFORMATION FOR SEQ ID NO: 8
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 4
US-10-155-059-10
; Sequence 10, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTI-BODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; INFORMATION FOR SEQ ID NO: 10
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;

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; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8

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```

Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

```

```

RESULT 4
US-10-155-059-10
; Sequence 10, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTI-BODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10

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Query Match          94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5
US-10-155-059-11
; Sequence 11, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-155-059-11
Query Match 94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 6
US-10-155-059-16
; Sequence 16, Application US/10155059
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
```

```
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-155-059-16
Query Match 94.3%; Score 99; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 7
US-08-244-476-18
; Sequence 18, Application US/08244476
; GENERAL INFORMATION:
; APPLICANT: Zentgraf, Hanswalter
; APPLICANT: Schranz, Peter
; APPLICANT: Volkmann, Martin
; APPLICANT: Tessmer, Claudia
; APPLICANT: Klein, Ralf
; TITLE OF INVENTION: METHOD OF DETECTING p53-SPECIFIC
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/244,476
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 94/08241
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 32 823.3
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18644-94281-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-244-476-18

Query Match 94.3%; Score 99; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 PPLSQETFSDLWKLLEN 21
| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-424-273-1
Sequence 1, Application US/08424273
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: P53 PROTEIN FRAGMENTS AND USE THEREOF FOR
TITLE OF INVENTION: DETECTING AND MONITORING DISEASED CONDITIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1 (ASC III)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,273
FILING DATE: 28-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9213110
FILING DATE: 2-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 9301082
FILING DATE: 2-NOV-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-08-424-273-1
Query Match 94.3%; Score 99; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 PPLSQETFSDLWKLLEN 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-10-155-059-14
Sequence 14, Application US/10155059
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-155-059-14

Query Match 89.5%; Score 94; DB 25; Length 20;
Best Local Similarity 94.4%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 PPLSQETFSDLWKLLEN 19
| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-10-155-059-15
Sequence 15, Application US/10155059
GENERAL INFORMATION:
APPLICANT: Kaelin, William


```
/ Jost, Christine
/
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/ NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/ ANTIBODIES
/
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/155,059
/ FILING DATE: 24-May-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/081,975
/ FILING DATE: 12-MAY-1998
/ APPLICATION NUMBER: 60/046,207
/ FILING DATE: 12-MAY-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Eisenstein, Ronald I
/ REGISTRATION NUMBER: 30,628
/ REFERENCE/DOCKET NUMBER: 47400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-345-6054
/ TELEFAX: 617-345-1300
/ TELEX: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
/
/ US-10-155-059-15
/
/ Query Match 89.5%; Score 94; DB 25; Length 20;
/ Best Local Similarity 94.4%; Pred. No. 4.3e-07;
/ Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
/
/ QY 1 PPLSQETFSDLWKLLPEN 18
/ | | | | | | | | | | | | | | | | | |
/ Db 2 PPLSQETFSDLWNLLEN 19
/
/ RESULT 11
/ US-09-214-371-73
/ Sequence 73, Application US/09214371B
/ GENERAL INFORMATION:
/ APPLICANT: Lane, David
/ APPLICANT: Bottger, Volker
/ APPLICANT: Bottger, Angelica
/ APPLICANT: Pickseley, Stephen
/ APPLICANT: Chene, Patrick
/ APPLICANT: Hochkeppel, Heinz-Kurt
/ APPLICANT: Garcia-Echeverria, Carlos
/ APPLICANT: Furet, Pascal
/
/ TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
/
/ FILE REFERENCE: 4-20937/A/PCT
/ CURRENT APPLICATION NUMBER: US/09/214,371B
/ CURRENT FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: PCT/EP97/03549
/ PRIOR FILING DATE: 1997-07-04
/ NUMBER OF SEQ ID NOS: 83
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 73
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/ LENGTH: 22
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
/ NAME/KEY: VARIANT
/ LOCATION: (1)
/ OTHER INFORMATION: X = Biotin-Ser
/
/ US-09-214-371-73
/
/ Query Match 88.6%; Score 93; DB 16; Length 22;
/ Best Local Similarity 100.0%; Pred. No. 6.9e-07;
/ Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 1 PPLSQETFSDLWKLLPE 17
/ | | | | | | | | | | | | | | | | | |
/ Db 6 PPLSQETFSDLWKLLPE 22
/
/ RESULT 12
/ US-09-732-384-7
/ Sequence 7, Application US/09732384
/ GENERAL INFORMATION:
/ APPLICANT: Yuan, Zhi-Min
/ APPLICANT: Gu, JiJie
/ TITLE OF INVENTION: Inhibition of p53 Degradation
/ FILE REFERENCE: 21508-044
/ CURRENT APPLICATION NUMBER: US/09/732,384
/ CURRENT FILING DATE: 2000-12-07
/ PRIOR APPLICATION NUMBER: 60/169,816
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Protein
/ OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
/
/ US-09-732-384-7
/
/ Query Match 87.6%; Score 92; DB 21; Length 19;
/ Best Local Similarity 100.0%; Pred. No. 8.4e-07;
/ Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 2 PLSQETFSDLWKLLPEN 18
/ | | | | | | | | | | | | | | | | | |
/ Db 1 PLSQETFSDLWKLLPEN 17
/
/ RESULT 13
/ US-10-155-059-13
/ Sequence 13, Application US/10155059
/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, William
/ APPLICANT: Jost, Christine
/
/ TITLE OF INVENTION: METHODS OF TREATMENT USING
/ NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
/ ANTIBODIES
/
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nixon Peabody LLP
/ STREET: 101 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/155,059
;; FILING DATE: 24-May-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/081,975
;; FILING DATE: 12-MAY-1998
;; APPLICATION NUMBER: 60/046,207
;; FILING DATE: 12-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eisenstein, Ronald I
;; REGISTRATION NUMBER: 30,628
;; REFERENCE/DOCKET NUMBER: 47400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-345-6054
;; TELEFAX: 617-345-1300
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13

Query Match 85.7%; Score 90; DB 25; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | |
Db 1 PLSQETFSDLWKLLPEN 18

RESULT 14

US-09-214-371-1
;; Sequence 1, Application US/09214371B
;; GENERAL INFORMATION:
;; APPLICANT: Lane, David
;; APPLICANT: Bottger, Volker
;; APPLICANT: Bottger, Angelica
;; APPLICANT: Pickaley, Stephen
;; APPLICANT: Chene, Patrick
;; APPLICANT: Hochkeppel, Heinz-Kurt
;; APPLICANT: Garcia-Echeverria, Carlos
;; APPLICANT: Furet, Pascal
;; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
;; FILE REFERENCE: 4-20937/A/PCT
;; CURRENT APPLICATION NUMBER: US/09/214,371B
;; CURRENT FILING DATE: 1999-03-26
;; PRIOR APPLICATION NUMBER: PCT/EP97/03549
;; PRIOR FILING DATE: 1997-07-04
;; NUMBER OF SEQ ID NOS: 83
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-1

Query Match 84.8%; Score 89; DB 16; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.5e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | |
Db 1* PLSQETFSDLWKLLPEN 17

RESULT 15

US-10-155-059-19
;; Sequence 19, Application US/10155059
;; GENERAL INFORMATION:
;; APPLICANT: Kaelin, William
;; Jost, Christine
;; TITLE OF INVENTION: METHODS OF TREATMENT USING
;; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
;; ANTIBODIES
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon Peabody LLP
;; STREET: 101 Federal Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSeq for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/155,059
;; FILING DATE: 24-May-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/081,975
;; FILING DATE: 12-MAY-1998
;; APPLICATION NUMBER: 60/046,207
;; FILING DATE: 12-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eisenstein, Ronald I
;; REGISTRATION NUMBER: 30,628
;; REFERENCE/DOCKET NUMBER: 47400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-345-6054
;; TELEFAX: 617-345-1300
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-155-059-19

Query Match 81.9%; Score 86; DB 25; Length 20;
Best Local Similarity 94.1%; Pred. No. 7.7e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | |
Db 3 PLSQETFSDLWKLLPPN 19

Search completed: February 12, 2003, 11:24:05
Job time : 378.625 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:15:02 ; Search time 12.6667 Seconds
(without alignments)
38.323 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 42882

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdb.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdb.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pdb.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdb.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pdb.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pdb.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	99	94.3	18	10	US-09-214-371-74
2	99	94.3	20	12	US-10-155-059-8
3	99	94.3	20	12	US-10-155-059-10
4	99	94.3	20	12	US-10-155-059-11
5	99	94.3	20	12	US-10-155-059-16
6	94	89.5	20	12	US-10-155-059-14
7	94	89.5	20	12	US-10-155-059-15
8	93	88.6	22	10	US-09-214-371-73
9	92	87.6	19	10	US-09-732-384-7
10	90	85.7	19	12	US-10-155-059-13
11	89	84.8	19	10	US-09-214-371-1
12	86	81.9	20	12	US-10-155-059-19
13	77	73.3	15	10	US-09-732-384-6
14	74	70.5	16	12	US-10-155-059-23
15	74	70.5	20	12	US-10-155-059-20
16	72	68.6	20	12	US-10-155-059-18
17	66	62.9	12	10	US-09-214-371-17
18	65	61.9	15	10	US-09-950-692-6
19	60	57.1	18	12	US-10-155-059-22

20	59	56.2	16	10	US-09-214-371-39	Sequence 39, Appl
21	57	54.3	14	9	US-10-024-123-7	Sequence 7, Appl
22	55	52.4	12	10	US-09-214-371-7	Sequence 7, Appl
23	54	51.4	12	10	US-09-214-371-24	Sequence 24, Appl
24	54	51.4	16	10	US-09-214-371-41	Sequence 41, Appl
25	53	50.5	16	10	US-09-214-371-40	Sequence 40, Appl
26	49	46.7	12	10	US-09-214-371-25	Sequence 25, Appl
27	49	46.7	12	10	US-09-214-371-26	Sequence 26, Appl
28	48	45.7	14	10	US-09-214-371-33	Sequence 33, Appl
29	48	45.7	14	10	US-09-214-371-34	Sequence 34, Appl
30	47	44.8	10	12	US-10-155-059-17	Sequence 17, Appl
31	47	44.8	16	10	US-09-019-679-3	Sequence 3, Appl
32	44	41.9	11	12	US-10-155-059-21	Sequence 21, Appl
33	44	41.9	12	10	US-09-214-371-20	Sequence 20, Appl
34	42	40.0	15	12	US-10-155-059-24	Sequence 24, Appl
35	36	34.3	6	10	US-09-214-371-83	Sequence 83, Appl
36	36	34.3	6	10	US-09-732-384-4	Sequence 4, Appl
37	36	34.3	6	12	US-10-155-059-1	Sequence 1, Appl
38	36	34.3	9	10	US-09-214-371-37	Sequence 37, Appl
39	36	34.3	9	10	US-09-214-371-38	Sequence 38, Appl
40	36	34.3	10	10	US-09-214-371-35	Sequence 35, Appl
41	36	34.3	10	10	US-09-214-371-36	Sequence 36, Appl
42	32	30.5	6	12	US-10-155-059-2	Sequence 2, Appl
43	32	30.5	12	9	US-09-840-277-66	Sequence 66, Appl
44	32	30.5	17	10	US-09-920-552-110	Sequence 110, App
45	31	29.5	8	10	US-09-214-371-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-214-371-74
; Sequence 74, Application US/09214371B
; Patent No. US2001001851A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botterger, Volker
; APPLICANT: Botterger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2
US-10-155-059-8
; Sequence 8, Application US/10155059
; Patent No. US20020147173A1

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;
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8
      94.3%; Score 99; DB 12; Length 20;
      Best Local Similarity 100.0%; Pred. No. 6.2e-09;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLKLPEN 18
    |||||
Db 2 PPLSQETFSDLWLKLPEN 19
    |||||

RESULT 3
US-10-155-059-10
; Sequence 10, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8
      94.3%; Score 99; DB 12; Length 20;
      Best Local Similarity 100.0%; Pred. No. 6.2e-09;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLKLPEN 18
    |||||
Db 2 PPLSQETFSDLWLKLPEN 19
    |||||

RESULT 4
US-10-155-059-11
; Sequence 11, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
```

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;
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10
      Query Match 94.3%; Score 99; DB 12; Length 20;
      Best Local Similarity 100.0%; Pred. No. 6.2e-09;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLKLPEN 18
    |||||
Db 2 PPLSQETFSDLWLKLPEN 19
    |||||

RESULT 4
US-10-155-059-11
; Sequence 11, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
```

REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-155-059-11

Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5
US-10-155-059-16
; Sequence 16, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-155-059-16

Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 6
US-10-155-059-14
; Sequence 14, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-155-059-14

Query Match 89.5%; Score 94; DB 12; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 7
US-10-155-059-15
; Sequence 15, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13

Db 1 PLSQOTFSDWLKLLPEN 17
RESULT 12
US-10-155-059-19
Sequence 19, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-155-059-19

Query Match 81.9%; Score 86; DB 12; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 3 PLSQOTFSDWLKLLPEN 19
RESULT 13
US-09-732-384-6
Sequence 6, Application US/09732384
Patent No. US20020132977A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, JiJie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816

Query Match 85.7%; Score 90; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSELNLLPEN 18

RESULT 11
US-09-214-371-1
Sequence 1, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pickseley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-1

Query Match 84.8%; Score 89; DB 10; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSDWLKLLPEN 18

RESULT 12
US-10-155-059-19
Sequence 19, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13

Query Match 81.9%; Score 86; DB 12; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 3 PLSQOTFSDWLKLLPEN 19
RESULT 13
US-09-732-384-6
Sequence 6, Application US/09732384
Patent No. US20020132977A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, JiJie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816

Query Match 85.7%; Score 90; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSELNLLPEN 18

RESULT 11
US-09-214-371-1
Sequence 1, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pickseley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-1

Query Match 84.8%; Score 89; DB 10; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSDWLKLLPEN 18

RESULT 12
US-10-155-059-19
Sequence 19, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13

Query Match 81.9%; Score 86; DB 12; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 3 PLSQOTFSDWLKLLPEN 19
RESULT 13
US-09-732-384-6
Sequence 6, Application US/09732384
Patent No. US20020132977A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, JiJie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816

Query Match 85.7%; Score 90; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSELNLLPEN 18

RESULT 11
US-09-214-371-1
Sequence 1, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pickseley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-1

Query Match 84.8%; Score 89; DB 10; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PLSQOTFSDWLKLLPEN 18
Db 1 PLSQOTFSDWLKLLPEN 18

;; PRIOR FILING DATE: 1999-12-08
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:Protein
;; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-6

Query Match 73.3%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLLPEN 18
Db 1 QETFSDLWKLLPEN 14

RESULT 14

US-10-155-059-23
; Sequence 23, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-155-059-23

Query Match 70.5%; Score 74; DB 12; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPE 17
Db 1 PLSQETFSDLWLSLLPD 16

RESULT 15

US-10-155-059-20
; Sequence 20, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
ANTIBODIES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997

ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-155-059-20

Query Match 70.5%; Score 74; DB 12; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLP 16
Db 3 PLSQETFSGLWKLLP 17

Search completed: February 12, 2003, 11:25:07
Job time : 12.6667 secs

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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:52 ; Search time 47.5 Seconds
(without alignments)
53.300 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PFLSQFTFSDLKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SID22/gcgdata/geneseq/geneseq-embl/AA1981.DAT:*
- 3: /SID22/gcgdata/geneseq/geneseq-embl/AA1982.DAT:*
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- 5: /SID22/gcgdata/geneseq/geneseq-embl/AA1984.DAT:*
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- 11: /SID22/gcgdata/geneseq/geneseq-embl/AA1990.DAT:*
- 12: /SID22/gcgdata/geneseq/geneseq-embl/AA1991.DAT:*
- 13: /SID22/gcgdata/geneseq/geneseq-embl/AA1992.DAT:*
- 14: /SID22/gcgdata/geneseq/geneseq-embl/AA1993.DAT:*
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- 18: /SID22/gcgdata/geneseq/geneseq-embl/AA1997.DAT:*
- 19: /SID22/gcgdata/geneseq/geneseq-embl/AA1998.DAT:*
- 20: /SID22/gcgdata/geneseq/geneseq-embl/AA1999.DAT:*
- 21: /SID22/gcgdata/geneseq/geneseq-embl/AA2000.DAT:*
- 22: /SID22/gcgdata/geneseq/geneseq-embl/AA2001.DAT:*
- 23: /SID22/gcgdata/geneseq/geneseq-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	99	94.3	25	AAW54907	Immunodominant epi
5	99	94.3	25	AAW51879	Human p53 amino ac
6	97	92.4	19	AAW47074	p53/RB interaction
7	93	88.6	22	AAW37227	p53 biotinylated N
8	81	77.1	15	AAW06310	Human p53 peptide
9	77	73.3	15	AAW54909	Immunodominant epi
10	77	73.3	15	AAW54910	Immunodominant epi

11	77	73.3	15	17	AAW89914	p53 protein bindin
12	77	73.3	15	21	AAW29157	Peptide #1. Unide
13	77	73.3	15	22	AAW89500	p53 DR 3a motif bi
14	77	73.3	15	22	AAW89730	p53 DR3 binding pe
15	77	73.3	17	20	AAW45227	p53 peptide 9-25.
16	74	70.5	15	21	AAW29159	Peptide #3. Unide
17	74	70.5	15	21	AAW29163	Peptide #7. Unide
18	73	69.5	14	23	ABW05528	Biotinylated pepi
19	73	69.5	15	21	AAW29167	Peptide #11. Unid
20	71	67.6	15	21	AAW29160	Peptide #4. Unide
21	71	67.6	15	21	AAW29161	Peptide #5. Unide
22	71	67.6	15	21	AAW99001	HLA class II bindi
23	70	66.7	13	21	AAW57799	TRAM-interaction m
24	69	65.7	15	21	AAW29162	Peptide #6. Unide
25	69	65.7	15	21	AAW29164	Peptide #8. Unide
26	66.5	63.3	16	21	AAW29149	Ligand #1. Uniden
27	66.5	63.3	16	21	AAW29158	Peptide #2. Unide
28	66	62.9	12	19	AAW37181	Human p53 wild-typ
29	66	62.9	12	19	AAW37188	Human oncogenic pr
30	66	62.9	12	21	AAW17075	Mdm/hdm antagonist
31	66	62.9	12	21	AAW17087	Mdm/hdm antagonist
32	66	62.9	12	23	ABW73170	Mdm/hdm antagonist
33	66	62.9	12	23	ABW73182	Mdm/hdm antagonist
34	66	62.9	16	19	AAW37201	Human oncogenic pr
35	65	61.9	15	16	AAW83012	Promega protein ki
36	65	61.9	15	21	AAW95859	Tumour suppressor
37	65	61.9	15	23	ABW09246	Target activatable
38	62	59.0	15	22	AAW89447	p53 DR supermotif
39	61	58.1	11	23	AAW52269	Miniature protein
40	61	58.1	12	19	AAW37190	Human oncogenic pr
41	61	58.1	12	21	AAW17077	Mdm/hdm antagonist
42	61	58.1	12	21	AAW17089	Mdm/hdm antagonist
43	61	58.1	12	23	ABW73172	Mdm/hdm antagonist
44	61	58.1	12	23	ABW73184	Mdm/hdm antagonist
45	61	58.1	16	19	AAW37203	Human oncogenic pr

ALIGNMENTS

RESULT 1
AAW82321
ID AAW82321 standard; Peptide; 19 AA.
XX
AC AAW82321;
XX
DT 22-FEB-1999 (first entry)
XX
DE p53 homologue TIP peptide.
XX
KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.
XX
OS Synthetic.
XX
FN WO9847919-A1.
XX
PD 29-OCT-1998.
XX
PF 20-APR-1998; 98WO-GB01140.
XX
PR 22-APR-1997; 97GB-0008089.
XX
PA (UYDU-) UNIV DUNDEE.
XX
PI Lane DP;
XX
DR WPI; 1998-609975/51.
XX
PT New substance with a mdm2 binding domain and coupling partner
PT useful for stabilising in cells without an efficient mdm2-mediated
PT degradation pathway
XX
PS Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds
 CC to mdm2. This peptide is used in the construction of a novel agent
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
 CC production of mdm2 in a population of cells. This agent is also used in
 CC the preparation of a therapeutic for activating p53, where the population
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53
 CC function. The agents for use in therapeutics for activating p53 can be
 CC used for the treatment of cancer, viral conditions or other conditions
 CC associated with non-functional p53.
 XX SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19
 |||||
 Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 2
 AAW82319
 ID AAW82319 standard; Peptide; 19 AA.

XX AC AAW82319;

XX DT 22-FEB-1999 (first entry)

XX DE p53 homologue TIP peptide.

XX KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX OS Synthetic.

XX PN WO9847525-A1.

XX PD 29-OCT-1998.

XX PF 20-APR-1998; 98WO-GB01144.

XX PR 22-APR-1997; 97GB-0008092.

XX PA (UYDU-) UNIV DUNDEE.

XX PI Lane DP;

XX DR WPI; 1998-609932/51.

XX PT New agents which inhibit interaction of p53 and mdm2 - useful for
 PT activating p53, e.g. for treating cancers, viral conditions or other
 PT conditions associated with non functional p53 or mdm2

XX FS Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds
 CC to mdm2. This peptide is used in the construction of a novel agent
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
 CC production of mdm2 in a population of cells. This agent is also used in
 CC the preparation of a therapeutic for activating p53, where the population
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53
 CC function. The agents for use in therapeutics for activating p53 can be
 CC used for the treatment of cancer, viral conditions or other conditions
 CC associated with non-functional p53.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19
 |||||
 Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 3
 AAW37228
 ID AAW37228 standard; peptide; 18 AA.

XX AC AAW37228;

XX DT 20-JUL-1998 (first entry)

XX DE p53 N-terminal peptide fragment for Elisa TIP assay.

XX KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumor; diagnosis; binding; viral infection; Elisa TIP assay.

XX OS Homo sapiens.

XX PN WO9801467-A2.

XX PD 15-JAN-1998.

XX PF 04-JUL-1997; 97WO-EP03549.

XX PR 07-APR-1997; 97GB-0007041.

XX PR 05-JUL-1996; 96GB-0014197.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PA (NOVS) NOVARTIS AG.

XX PI Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;
 PI Hochkeppel H, Lane D, Pickaley S;

XX DR WPI; 1998-100996/09.

XX PT Compounds binding to MDM2 protein and inhibit its interaction with
 PT p53 - useful in, e.g. diagnosis and treatment of cancer and viral
 PT infections and identifying binding agents

XX PS Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP
 CC assay for analysing the interaction between human oncogenic protein MDM2
 CC and p53. The invention provides peptide derivatives capable of binding to
 CC the human MDM2. These peptides can specifically inhibit or block the
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting
 CC the interaction between the p53 and MDM2 can induce growth arrest or
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated
 CC levels of MDM2. The peptides may be used to identify molecules that bind
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They
 CC may also be used to purify binding partners especially MDM2, diagnose
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia
 CC patients and for treatment or prevention of disease involving p53/MDM2
 CC interactions, especially tumours and viral infections. The peptides can
 CC be administered nasally, rectally, orally or by injection. By interfering
 CC with MDM2/p53 interaction, the peptides can activate p53 function and
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding
 CC site in p53, have a significantly greater blocking activity compared
 CC with wild-type p53.

XX SQ Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPEN 18
 |||||

Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 4

AA54907

ID AAR54907 standard; peptide; 25 AA.

XX AC AAR54907;

XX DT 29-NOV-1994 (first entry)

XX DE Immunodominant epitope from p53 N-terminal.

XX KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;

XX KW immunodominant epitope; human cellular tumour antigen;

XX KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EURO BIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX DR WPI; 1994-167463/20.

XX PT New immuno-dominant epitope(s) of protein p53 - for detecting and

XX PT monitoring antibodies indicative of cancer and precancerous

XX PT states

XX PS Claim 4; Page 42; 62pp; French.

XX CC Peptides derived from the N-terminal (amino acids 1-112) or the C-

XX CC terminal (amino acids 350-393) of protein p53 which specifically

XX CC react with anti-p53 antibodies in patients with cancer or

XX CC precancerous conditions are claimed. The peptides (AAR54907-R54921)

XX CC are useful for detecting and monitoring cancerous and precancerous

XX CC conditions.

XX SQ Sequence 25 AA;

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5

AAR51879

ID AAR51879 standard; Protein; 25 AA.

XX AC AAR51879;

XX DT 18-NOV-1994 (first entry)

XX DE Human p53 amino acids 9-33.

XX KW Human nuclear phosphoprotein p53; tumour suppressor gene product;

XX KW anti-oncogene; cancer; tumour; antibody binding region; epitope.

XX OS Homo sapiens.

XX PN WO9408241-A.

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 6

AAW47074

ID AAW47074 standard; peptide; 19 AA.

XX AC AAW47074;

XX DT 19-MAY-1998 (first entry)

XX DE p53/RB interaction inhibiting peptide 6 (residues 11-29 of human p53).

XX KW Retinoblastoma gene; RB; p53 protein; interaction; inhibitor;

XX KW tumour; apoptosis; modulator; medicine; veterinary; human.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9741433-A1.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-GB01168.

XX PR 29-APR-1996; 96GB-0008937.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PI Kouzarides T;

XX DR WPI; 1997-549887/50.

XX PT Identifying compounds that modulate interaction of p53 and Rb

XX PT protein - or those that bind to Rb protein, used to induce

XX PT apoptosis, specifically for treatment of tumours

XX PS Claim 36; Page 63; 83pp; English.

Query Match 94.3%; Score 99; DB 15; Length 25;

Best Local Similarity 100.0%; Pred. No. 7.1e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 4 PPLSQETFSDLWKLLPEN 21

XX This peptide fragment of p53 is an inhibitor of the interaction between
 CC a p53 protein and a retinoblastoma (RB) protein. This peptide
 CC corresponds to residues 11-29 of human p53 (AAW47079). The interaction
 CC between p53 and Rb is found to be critical for determining whether or not
 CC a cell enters apoptosis. Apoptosis is prevented if interaction occurs.
 CC The interaction is between regions 1-71 or 290-393 of p53 and region
 CC 379-928 of Rb. The invention provides methods to identify compounds able
 CC to modulate interaction or binding between p53 and Rb protein. The method
 CC comprises combining p53 and Rb, or their fragments, with a test compound
 CC and detecting interaction/binding between them. These inhibitory
 CC compounds are used in human or veterinary medicine to modulate p53
 CC activity and processes, specifically for inducing apoptosis in tumour
 CC cells (possibly also in cells infected by virus), in vivo or in vitro.
 CC Expression of these modulators by gene therapy methods is also
 CC contemplated. Other activities that can be affected are transcription
 CC repression, G1 arrest, DNA repair, homologous recombination and
 CC 3'-5'-exonuclease activity. Modulation of interaction with Rb may also
 CC stabilise p53.

XX SQ Sequence 19 AA;

Query Match 92.4%; Score 97; DB 18; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.1e-08;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLEN 19

RESULT 7
 AAW37227
 ID AAW37227 standard; peptide; 22 AA.

XX AC AAW37227;

XX DT 20-JUL-1998 (first entry)

XX DE p53 biotinylated N-terminal peptide fragment for Elisa P2 assay.

XX KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 KW tumour; diagnosis; binding; viral infection; Elisa P2 assay.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "biotinylated"

XX PN WO9801467-A2.

XX PD 15-JAN-1998.

XX PF 04-JUL-1997; 97WO-EP03549.

XX PR 07-APR-1997; 97GB-0007041.

XX PR 05-JUL-1996; 96GB-0014197.

XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA (NOVS) NOVARTIS AG.

XX PI Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;

XX PI Hochkeppel H, Lane D, Pickles S;

XX DR WPI; 1998-100996/09.

XX FT Compounds binding to MDM2 protein and inhibit its interaction with
 FT p53 - useful in, e.g. diagnosis and treatment of cancer and viral
 FT infections and identifying binding agents

XX PS Disclosure; Page 34; 45pp; English.

CC This p53 biotinylated N-terminal peptide fragment is used in an Elisa P2
 CC assay for analysing the interaction between human oncogenic protein MDM2
 CC and p53. The invention provides peptide derivatives capable of binding to
 CC the human MDM2. These peptides can specifically inhibit or block the
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting
 CC the interaction between the p53 and MDM2 can induce growth arrest or
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated
 CC levels of MDM2. The peptides may be used to identify molecules that bind
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They
 CC may also be used to purify binding partners especially MDM2, diagnose
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia
 CC patients and for treatment or prevention of disease involving p53/MDM2
 CC interactions, especially tumours and viral infections. The peptides can
 CC be administered nasally, rectally, orally or by injection. By interfering
 CC with MDM2/p53 interaction, the peptides can activate p53 function and
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding
 CC site in p53, have a significantly greater blocking activity compared
 CC with wild-type p53.

XX SQ Sequence 22 AA;

Query Match 88.6%; Score 93; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLE 17
 |||||
 Db 6 PPLSQETFSDLWKLLE 22

RESULT 8
 AAY06310
 ID AAY06310 standard; Peptide; 15 AA.

XX AC AAY06310;

XX DT 06-SEP-1999 (first entry)

XX DE Human p53 peptide (aa13-27).

XX KW RB18A; p53 regulatory protein; apoptosis; neoplasia; inflammation;
 KW wound healing; graft rejection; reperfusion injury;
 KW myocardial infarction; stroke; traumatic brain injury;
 KW neurodegenerative disease; ischaemia; toxemia; infection; AIDS;
 KW hepatitis; breast cancer; ovarian cancer; colon cancer; diagnosis;
 KW therapy; human.

XX OS Homo sapiens.

XX PN WO9931231-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-EP08560.

XX PR 15-DEC-1997; 97EP-0403051.

XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Frade R;

XX DR WPI; 1999-395177/33.

XX PT New p53 regulatory protein (RB18A) useful as, e.g. sources of probes
 PT and primers to detect the transcription rate and abundance of RB18A
 PT mRNA in lymphocytes

XX PS Example 1; Page 25; 87pp; English.

XX CC This synthetic peptide corresponds to amino acids 13-27 of human
 CC p53. It was used to raise anti-peptide p53.1 and anti-RB18A
 CC antibodies in rabbit. RB18A (see AAY06310) is a novel p53
 CC regulatory protein of the invention. The antibodies were used in

CC immunoscreenings that led to the isolation of a cDNA clone (see
 CC AAX59124) encoding human RB18A. The invention provides methods and
 CC compositions for the diagnostic and therapeutic applications of
 CC RB18A, in particular for the diagnosis, prevention or treatment of
 CC neoplasia.

XX SQ Sequence 15 AA;

Query Match 77.1%; Score 81; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLP 16
 | | | | | | | | | | | | | | | |
 Db 1 PLSQETFSDLWKLLP 15

RESULT 9

AAR54909
 ID AAR54909 standard; peptide; 15 AA.

XX AC
 XX AC
 XX AC

DT 29-NOV-1994 (first entry)

DE Immunodominant epitope from p53 N-terminal.

XX cancer; pre-cancerous state; detection; diagnosis; human p53 gene;
 KW immunodominant epitope; human cellular tumour antigen;
 KW transformation-associated protein.

OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EUROBIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX WPI; 1994-167463/20.

XX New immuno:dominant epitope(s) of protein p53 - for detecting and
 PT monitoring antibodies indicative of cancer and precancerous
 PT states

XX PS Claim 5; Page 42; 62pp; French.

XX Peptides derived from the N-terminal (amino acids 1-112) or the C-
 CC terminal (amino acids 350-393) of protein p53 which specifically
 CC react with anti-p53 antibodies in patients with cancer or
 CC precancerous conditions are claimed. The peptides (AAR54907-R54921)
 CC are useful for detecting and monitoring cancerous and precancerous
 CC conditions.

XX SQ Sequence 15 AA;

Query Match 73.3%; Score 77; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKL 14
 | | | | | | | | | | | | | | | |
 Db 2 PPLSQETFSDLWKL 15

RESULT 10

AAR54910

ID AAR54910 standard; peptide; 15 AA.

XX AC
 XX AC
 XX AC

DT 29-NOV-1994 (first entry)

XX Immunodominant epitope from p53 N-terminal.

XX cancer; pre-cancerous state; detection; diagnosis; human p53 gene;
 KW immunodominant epitope; human cellular tumour antigen;
 KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

XX PD 11-MAY-1994.

XX PF 02-NOV-1993; 93WO-FR01082.

XX PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EUROBIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX WPI; 1994-167463/20.

XX New immuno:dominant epitope(s) of protein p53 - for detecting and
 PT monitoring antibodies indicative of cancer and precancerous
 PT states

XX PS Claim 5; Page 42; 62pp; French.

XX Peptides derived from the N-terminal (amino acids 1-112) or the C-
 CC terminal (amino acids 350-393) of protein p53 which specifically
 CC react with anti-p53 antibodies in patients with cancer or
 CC precancerous conditions are claimed. The peptides (AAR54907-R54921)
 CC are useful for detecting and monitoring cancerous and precancerous
 CC conditions.

XX SQ Sequence 15 AA;

Query Match 73.3%; Score 77; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLLPEN 18
 | | | | | | | | | | | | | | | |
 Db 1 QETFSDLWKLLPEN 14

RESULT 11

AAR89914

ID AAR89914 standard; peptide; 15 AA.

XX AC
 XX AC
 XX AC

DT 10-SEP-1996 (first entry)

XX p53 protein binding motif corresp. to residues 16-30.

XX Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
 KW inhibition; diagnosis; treatment; malignancy; consensus.

XX OS Synthetic.

XX PN WO9602642-A1.

XX PD 01-FEB-1996.

XX PF 20-JUL-1995; 95WO-GB01719.

PR 19-APR-1995; 95US-0424957.
 XX 20-JUL-1994; 94US-0277660.
 PA (UYDU-) UNIV DUNDEE.
 PI Lane DP, Pickesley SM;
 XX WPI; 1996-105905/11.
 DR New cpds. which interfere with binding of MDM2 and p53 - used to
 PT develop prods. for use in the diagnosis and treatment of cancer and
 PT other malignancies
 XX
 XX Disclosure; Page 1; 46pp; English.
 XX
 CC New peptides of the invention which interfere with the binding of the
 CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
 CC the peptide sequences AAR89911-3 which form part of the p53 protein
 CC binding motif between amino acids 16-33 (AAR89914). The peptides were
 CC identified by modifying the p53 consensus binding sequence by
 CC substitution of an Alanine at each pos. and identifying which amino
 CC acid changes altered binding to expressed MDM2. The peptides and
 CC methods of identifying similar inhibitory peptides can be used to
 CC diagnose and treat e.g. cancer and other malignancies.
 XX
 XX Sequence 15 AA;
 SQ

Query Match 73.3%; Score 77; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWLKLPEN 18
 DB 1 QETFSDLWLKLPEN 14
 |||||

RESULT 12
 AAB29157
 ID AAB29157 standard; Peptide; 15 AA.
 AC AAB29157;
 XX
 XX 02-FEB-2001 (first entry)
 DT
 XX Peptide #1.
 DE
 XX Fork head associated; FHA; domain; transcriptional control;
 KW DNA replication; DNA repair; cell cycle control.
 XX Unidentified.
 OS
 XX WO200057184-A2.
 PN
 XX 28-SEP-2000.
 PD
 XX
 XX 17-MAR-2000; 2000WO-GB01024.
 PF
 XX 19-MAR-1999; 99GB-0006432.
 PR
 XX 28-JUN-1999; 99GB-0015075.
 PR
 XX (KUDO-) KUDOS PHARM LTD.
 PA
 XX Jackson SP, Durocher D;
 PI
 XX WPI; 2000-664872/64.
 DR
 XX Assays and screening methods based on direct interaction between FHA
 PT domains and phosphopeptides, useful for characterizing binding and to
 PT identify binding partners and modulators of FHA domain-phosphopeptide
 PT binding -
 XX
 XX Disclosure; Fig 2; 92pp; English.
 PS
 XX

CC The present invention relates to assays and screening methods based on
 CC a direct interaction between fork head associated (FHA) domains and
 CC phosphorylated polypeptides, for characterizing the binding of these
 CC molecules. FHA peptides may be useful for treating medical conditions
 CC associated with defects in transcriptional control, DNA replication,
 CC DNA repair, cell cycle control or other cellular process. The method
 CC may provide valuable insights into checkpoint signalling, has important
 CC implications for the functions of other FHA domain-containing
 CC proteins and provides basis for new lines of therapy. The present
 CC sequence is a peptide used in the present invention.
 XX

SQ Sequence 15 AA;

Query Match 73.3%; Score 77; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWLK 14
 |||||

DB 2 PPLSQETFSDLWLK 15
 |||||

RESULT 13

AAG89500

ID AAG89500 standard; Peptide; 15 AA.

XX

AC AAG89500;

XX

DT 11-SEP-2001 (first entry)

XX

DE p53 DR 3a motif binding peptide exemplary sequence #3.

XX

KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;

KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;

KW vaccine; epitope; cytostatic.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200141788-A1.

XX

PD 14-JUN-2001.

XX

PF 11-DEC-2000; 2000WO-US33629.

XX

PR 10-DEC-1999; 99US-0458297.

XX

PA (EPIM-) EPIMUNE INC.

XX

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;

PI Keogh E;

XX

DR WPI; 2001-381493/40.

XX

PT Epitope-based vaccines comprising p53 epitope having a specified

PT sequences, useful for treating and preventing cancer, the epitopic

PT peptides is useful as diagnostic agents and for evaluating immune

PT response -

XX

PS Disclosure; Page 113; 138pp; English.

XX

CC The present invention describes isolated prepared p53 epitopes (I). Also
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a
 CC vaccine composition comprising (II), a unit dose of a peptide with less
 CC than 50 contiguous amino acids with 100% identity to the native peptide
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
 CC has cytostatic activity and can be used in vaccines. The vaccine
 CC composition is useful for treating or preventing cancer. (I) and (II)
 CC are useful as diagnostic agents and for evaluating immune responses.
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be

CC present in whole antigens can be avoided with the use of the vaccine
CC composition of (I). The ability to combine selected epitopes and
CC further, to modify the composition of the epitopes enhances the
CC immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigens, which might have their own
CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
CC represent amino acid sequences used in the exemplification of the
CC present invention.
XX Sequence 15 AA;
SQ Query Match 73.3%; Score 77; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
Db 2 PPLSQETFSDLWKL 15

RESULT 14
AAG89730
ID AAG89730 standard; Peptide; 15 AA.
XX AC AAG89730;
XX DT 11-SEP-2001 (first entry)
XX DE p53 DR3 binding peptide #1.
XX Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
KW vaccine; epitope; cytostatic.
XX Homo sapiens.
OS Synthetic.
XX WO200141788-A1.
XX 14-JUN-2001.
XX PF 11-DEC-2000; 2000WO-US33629.
XX PR 10-DEC-1999; 99US-0458297.
XX PA (EPIM-) EPIMUNE INC.
XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX WPI; 2001-381493/40.
XX Epitope-based vaccines comprising p53 epitope having a specified
PT sequences, useful for treating and preventing cancer, the epitopic
PT peptides is useful as diagnostic agents and for evaluating immune
PT response -
XX Example 5; Page 131; 138pp; English.
XX The present invention describes isolated prepared p53 epitopes (I). Also
CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
CC and a second epitope and has less than 50 contiguous amino acids; (3) a
CC vaccine composition comprising (II), a unit dose of a peptide with less
CC than 50 contiguous amino acids with 100% identity to the native peptide
CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
CC has cytostatic activity and can be used in vaccines. The vaccine
CC composition is useful for treating or preventing cancer. (I) and (II)
CC are useful as diagnostic agents and for evaluating immune responses.
CC Unlike conventional epitopes, immunosuppressive epitopes that may be
CC present in whole antigens can be avoided with the use of the vaccine
CC composition of (I). The ability to combine selected epitopes and

CC further, to modify the composition of the epitopes enhances the
CC immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigens, which might have their own
CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
CC represent amino acid sequences used in the exemplification of the
CC present invention.
XX Sequence 15 AA;
SQ Query Match 73.3%; Score 77; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
Db 2 PPLSQETFSDLWKL 15

RESULT 15
AAY45227
ID AAY45227 standard; peptide; 17 AA.
XX AC AAY45227;
XX DT 06-JAN-2000 (first entry)
XX DE p53 peptide 9-25.
XX Immunisation; immunogenicity enhancer; rabies virus strain ERA;
KW immunodominant T-helper cell determinant; nucleoprotein; antibody;
KW post-translational modification; p53; cancer; diagnosis.
XX Synthetic.
XX WO9946574-A2.
XX 16-SEP-1999.
XX PF 11-MAR-1999; 99WO-US04653.
XX PR 11-MAR-1998; 98US-0077512.
XX PA (WIST-) WISTAR INST.
XX Otvos L, Ertl H, Thurin M, Hoffman R;
XX WPI; 1999-561693/47.
XX Methods of detecting post-translational modification level of p53,
PT useful for diagnosis of cancer -
XX Disclosure; Page 45; 59pp; English.
XX The present invention describes a polypeptide comprising a portion of a
CC p53 comprising a post-translationally modified amino acid residue where
CC the modification is a phosphorylation, glycosylation or prenylation, and
CC an immunogenicity enhancer. The polypeptide is used to detect anti-p53
CC autoantibodies in a human patient. The antibody can be used to determine
CC the post-translational modification state of a p53 protein. These are
CC used especially in the diagnosis of cancer. The present sequence
CC represents a p53 peptide used in the exemplification of the present
CC invention.
XX Sequence 17 AA;
SQ Query Match 73.3%; Score 77; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
Db 4 PPLSQETFSDLWKL 17

Search completed: February 12, 2003, 11:13:44
Job time : 47.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:02 ; Search time 37.2083 Seconds
(without alignments)
105.216 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLKLPENG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertibrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	77	73.3	25	4 Q9NP68	Q9np68 homo sapien
2	45	42.9	22	13 Q9W6D7	Q9w6d7 gallus gall
3	33	31.4	24	13 Q90Z19	Q90z19 gallus gall
4	33	31.4	24	15 Q85618	Q85618 avian leuko
5	32	30.5	19	5 P83003	P83003 entamoeba h
6	32	30.5	25	2 Q9S0U6	Q9s0u6 shigella so
7	31	29.5	16	6 Q9BGH8	Q9bg8 sorex arane
8	31	29.5	24	5 Q94377	Q94377 caenorhabdi
9	30	28.6	14	6 Q77538	Q77538 bos taurus
10	30	28.6	23	4 Q9HCW9	Q9hcw9 homo sapien
11	30	28.6	24	5 Q94368	Q94368 caenorhabdi
12	29	27.6	17	8 Q9XNQ1	Q9xng1 boophilus m
13	29	27.6	24	5 Q95V74	Q95v74 mytilus gal
14	28.5	27.1	24	3 P87182	P87182 trichoderma
15	28	26.7	20	10 Q9LKD5	Q9lkd5 citrus sine
16	28	26.7	20	12 Q912B4	Q912b4 human eryth

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17 28 26.7 21 6 Q9N1C9
18 28 26.7 24 6 Q9TUP6
19 27.5 26.2 22 2 Q53422
20 27 25.7 11 4 Q9UEU0
21 27 25.7 24 2 Q9R3J2
22 26 24.8 14 10 P82326
23 26 24.8 17 11 Q9QVS7
24 26 24.8 18 4 Q9UJZ3
25 26 24.8 20 6 Q95MK2
26 26 24.8 20 6 Q95MK1
27 26 24.8 20 6 Q95MK0
28 26 24.8 20 6 Q95MJ9
29 26 24.8 20 6 Q95MJ8
30 26 24.8 20 6 Q95MJ7
31 26 24.8 20 10 Q988Y7
32 26 24.8 22 2 Q9RSU3
33 26 24.8 22 8 Q9TLD2
34 26 24.8 22 12 Q64831
35 26 24.8 23 4 Q14347
36 25 23.8 16 12 Q83960
37 25 23.8 17 2 Q9F0P3
38 25 23.8 18 6 P82674
39 25 23.8 18 12 Q84129
40 25 23.8 19 10 Q22064
41 25 23.8 19 12 Q83965
42 25 23.8 20 2 Q9R502
43 25 23.8 20 6 Q95MK6
44 25 23.8 20 6 Q95MK5
45 25 23.8 20 6 Q95MK4

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ALIGNMENTS

RESULT 1

```

Q9NP68 PRELIMINARY; PRT; 25 AA.
ID Q9NP68
AC Q9NP68;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Tumor suppressor p53 (Fragment).
GN TP53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209136; AAF36354.1; -
DR EMBL; AF209128; AAF36354.1; -
DR EMBL; AF209129; AAF36355.1; -
DR EMBL; AF209130; AAF36356.1; -
DR EMBL; AF209131; AAF36357.1; -
DR EMBL; AF209132; AAF36358.1; -
DR EMBL; AF209133; AAF36359.1; -
DR EMBL; AF209134; AAF36360.1; -
DR EMBL; AF209135; AAF36361.1; -
DR InterPro; IPR002117; P53.
DR NON_TER
FT NON_TER 25
SQ SEQUENCE 25 AA; 2890 MW; D7FA272EBFAB9798 CRC64;

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Query Match 73.3%; Score 77; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWLK 14

DB 12 PPLSQETFSDLWLK 25

```
RESULT 2
Q9W6D7 PRELIMINARY; PRT; 22 AA.
ID AC Q9W6D7
AC Q9W6D7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hydroxyindole-o-methyltransferase isoform A (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9067015; PubMed=9851690;
RA Grechez-Cassiau A., Bernard M., Ladjali K., Rodriguez I.R., Voisin P.;
RT "Structural analysis of the chicken hydroxyindole-O-methyltransferase
gene."
RL Eur. J. Biochem. 258:44-52(1998).
DR EMBL; AF116455; AAD23444.1; -.
DR Methylytransferase; Transferase.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;

Query Match 42.9%; Score 45; DB 13; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.5;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKL 15
Db 8 SQHGFADLWELM 19

RESULT 3
Q90ZJ9 PRELIMINARY; PRT; 24 AA.
ID AC Q90ZJ9
AC Q90ZJ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE C-myc oncogene, aa 44-62 from c-myc/LL3 (ALV provirus)
DE (Fragment)
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84144799; PubMed=6322173;
RA Westaway D., Payne G., Varmus H.E.;
RT "Proviral deletions and oncogene base-substitutions in insertionally
mutagenized c-myc alleles may contribute to the progression of avian
bursal tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
DR EMBL; K01440; AAA48964.1; -.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF01056; Myc_N_term; 1.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match 31.4%; Score 33; DB 13; Length 24;
Best Local Similarity 47.4%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 2;

Qy 4 SQETFSDLWKL 15
Db 8 SQHGFADLWELM 19

RESULT 4
Q85618 PRELIMINARY; PRT; 24 AA.
ID AC Q85618
AC Q85618;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE RAV-2 proviral DNA, c-myc (Aa 44-67), allele LL3 (Fragment).
OS Avian leukosis virus.
OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11864;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84144799; PubMed=6322173;
RA Westaway D., Payne G., Varmus H.E.;
RT "Proviral deletions and oncogene base-substitutions in insertionally
mutagenized c-myc alleles may contribute to the progression of avian
bursal tumors."
RL Proc. Natl. Acad. Sci. U.S.A. 81:843-847(1984).
DR EMBL; K01439; AAA51600.1; -.
DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF01056; Myc_N_term; 1.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2679 MW; 93F59F2D3B24E527 CRC64;

Query Match 31.4%; Score 33; DB 15; Length 24;
Best Local Similarity 47.4%; Pred. No. 2.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 2;

Qy 1 PPLSOETFSDLWK--LLP 16
Db 2 PPAPSE--DIWKKFELLP 17

RESULT 5
P83003 PRELIMINARY; PRT; 19 AA.
ID AC P83003
AC P83003;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Calreticulin-like protein (Fragment).
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE.
RC STRAIN=HM-1:IMMS;
RA Gonzalez E., Mendoza G., Ramos F., Garcia G., Moran P., Valadez A.,
RA Zaragoza M.E., Melendro E.I., Ximenez C.;
RT "Calreticulin-like molecule in trophozoites of Histolytica HM1-IMMS."
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- DEVELOPMENTAL STAGE: IN TROPHOZOITES.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2488 MW; FC90BCAEFE1BA764 CRC64;

Query Match 30.5%; Score 32; DB 5; Length 19;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QETFSDLWKL 15
Db 5 EETFGWKXI 15
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RESULT 6
Q9S0U6 PRELIMINARY; PRT; 25 AA.
ID Q9S0U6;
AC Q9S0U6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF108 (Fragment).
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OC NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HW383;
RA Chida T., Okamura N., Ohtani K., Yoshida Y., Arakawa E., Watanabe H.;
RT "The complete DNA sequence of the O antigen gene region of Plesiomonas
RT shigelloides serotype O17 which is identical to Shigella sonnei form
RT I antigen.";
RN Microbiol. Immunol. 44:161-172(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=HW383;
RX MEDLINE=99036814; PubMed=9817819;
RA Hough H.H., Venkatesan M.M.;
RT "Genetic analysis of Shigella sonnei form I antigen: identification of
RT a novel IS630 as an essential element for the form I antigen
RT expression";
RL Microb. Pathog. 25:165-173(1998).
DR EMBL; AB028134; BAA85070.1; -.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2726 MW; A6CC5D24211CDAAD CRC64;

Query Match 30.5%; Score 32; DB 2; Length 25;
Best Local Similarity 42.9%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKL 15
Db 4 PPSAEFFGTFWLVL 17

RESULT 7
Q9BGG8 PRELIMINARY; PRT; 16 AA.
ID Q9BGG8;
AC Q9BGG8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 17 of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1951 MW; 775186E3FE5F52E2 CRC64;

Query Match 29.5%; Score 31; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 8
Q94377 PRELIMINARY; PRT; 24 AA.
ID Q94377;
AC Q94377;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PPI-like Ser/Thr protein phosphatase (fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC Zeke T., Gergely P., Dombradi V.;
RT "The catalytic subunits of Ser/Thr protein phosphatases from
RT Caenorhabditis elegans: A biochemical and molecular biological
RT survey.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR EMBL; Z77740; CAB01299.1; -.
DR HSPSP; P08129; IPRJ.
DR InterPro; IPR004844; S/T_phosphatse.
DR ProDom; PD000252; S/T_phosphatse; 1.
KW Hydrolase; Iron; Manganese.
FT NON_TER 1
FT NON_TER 24
SQ SEQUENCE 24 AA; 2816 MW; 2BF73DBB5F20359 CRC64;

Query Match 29.5%; Score 31; DB 5; Length 24;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 PSDLWKLPPENG 19
Db 2 YSLLRIFDKNG 13

RESULT 9
Q77538 PRELIMINARY; PRT; 14 AA.
ID Q77538;
AC Q77538;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRED HOLSTEIN;
RX MEDLINE=99175163; PubMed=10075683;
RA Jiang H., Okamura C.S., Lucy M.C.;
RT "Isolation and characterization of a novel promoter for the bovine
RT growth hormone receptor gene.";
RL J. Biol. Chem. 274:7893-7900(1999).

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RN [3]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
  receptor mRNA."; 1997 to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Jiang H., Lucy M.C.;
RA "Bovine GH receptor 5' UTR variants.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036297; AAC33315.2; -
DR EMBL; AF085281; AAC33308.1; -
DR EMBL; AF036290; AAC33309.1; -
DR EMBL; AF036291; AAC33310.1; -
DR EMBL; AF036292; AAC33311.1; -
DR EMBL; AF036293; AAC33312.1; -
DR EMBL; AF036294; AAC33313.1; -
DR EMBL; AF036295; AAC33314.1; -
DR EMBL; AF036296; AAC33315.1; -
DR EMBL; AF326349; AAC97345.1; -
KW Receptor.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1544 MW; 5A45D458FF3A9E27 CRC64;

Query Match 28.6%; Score 30; DB 6; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLWKLL 15
   |||:|
Db 2 DLWQLL 7

RESULT 10
Q9HCW9 PRELIMINARY; PRT; 23 AA.
AC Q9HCW9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Orlovsky I.V., Sverdlova P.S., Rubtsov P.M.;
RT "Microsatellites within the human growth hormone receptor gene.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295613; CAC06615.1; -
KW Receptor.
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2426 MW; 9A0833A0F1DD699E CRC64;

Query Match 28.6%; Score 30; DB 4; Length 23;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DLWKLL 15
   |||:|
Db 2 DLWQLL 7

RESULT 11
Q94368 PRELIMINARY; PRT; 24 AA.
AC Q94368;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE PPI-like Ser/Thr protein phosphatase (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeke T., Gergely P., Dombradi V.;
RT "The catalytic subunits of Ser/Thr protein phosphatases from
  Caenorhabditis elegans: A biochemical and molecular biological
  survey.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
  PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES.
DR EMBL; Z77728; CAB01287.1; -.
DR HSSP; P08129; IFJM.
DR InterPro; IPR004844; S/T_phosphatse.
DR ProDom; PD000252; S/T_phosphatse; 1.
KW Hydrolase; Iron; Manganese.
FT NON_TER 1 1
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2781 MW; 353E423EA763AA75 CRC64;

Query Match 28.6%; Score 30; DB 5; Length 24;
Best Local Similarity 58.3%; Pred. No. 7.5e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 FSDLWKLLPENG 19
   |||:|
Db 2 YSDDLALLELNG 13

RESULT 12
Q9XNQ1 PRELIMINARY; PRT; 17 AA.
AC Q9XNQ1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COLI.
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
  Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110614; AAD28397.1; -.
KW Mitochondrion.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1988 MW; 319F2D4D7DA11F3 CRC64;

Query Match 27.6%; Score 29; DB 8; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SQETFSDL 11
   |||:|
Db 5 SQTFSDM 12

RESULT 13
Q95V74 PRELIMINARY; PRT; 24 AA.
ID Q95V74
AC Q95V74;

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DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Elongation factor 1 alpha (Fragment).
 OS Mytilus galloprovincialis (Mediterranean mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=29158;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pierre N., Daguin C., Borsa P., Jollivet D., Viard F., Bonhomme F.,
 RA David P.;
 RT "Introgession patterns in the Mytilus edulis / Mytilus
 RT galloprovincialis mosaic hybrid zone along the Atlantic coasts of
 RT France.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF424742; AAL24803.1; -
 FT NON_TER 1
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2875 MW; 1D0DEAD3FBD13DCB CRC64;

 Query Match 27.6%; Score 29; DB 5; Length 24;
 Best Local Similarity 38.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 Qy 1 PPLSQETFSDLWK 13
 Db 4 PPYSEARFMEIOK 16

 RESULT 14
 P87182
 ID P87182 PRELIMINARY; PRT; 24 AA.
 AC P87182;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Carbamoyl phosphate synthetase, small subunit (arg2).
 OS Trichoderma virens.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_TaxID=29875;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baek J.-M., Kenerley C.M.;
 RT "The arg2 gene of Trichoderma virens: Cloning and development of a
 RT homologous transformation system.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001029; AAB58298.1; -
 SQ SEQUENCE 24 AA; 2782 MW; 8FPD15C27EAD244C CRC64;

 Query Match 27.1%; Score 28.5; DB 3; Length 24;
 Best Local Similarity 53.8%; Pred. No. 1.3e+03;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

 Qy 4 SQETFSO-LWKLL 15
 Db 10 SDYLSDLWAL 22

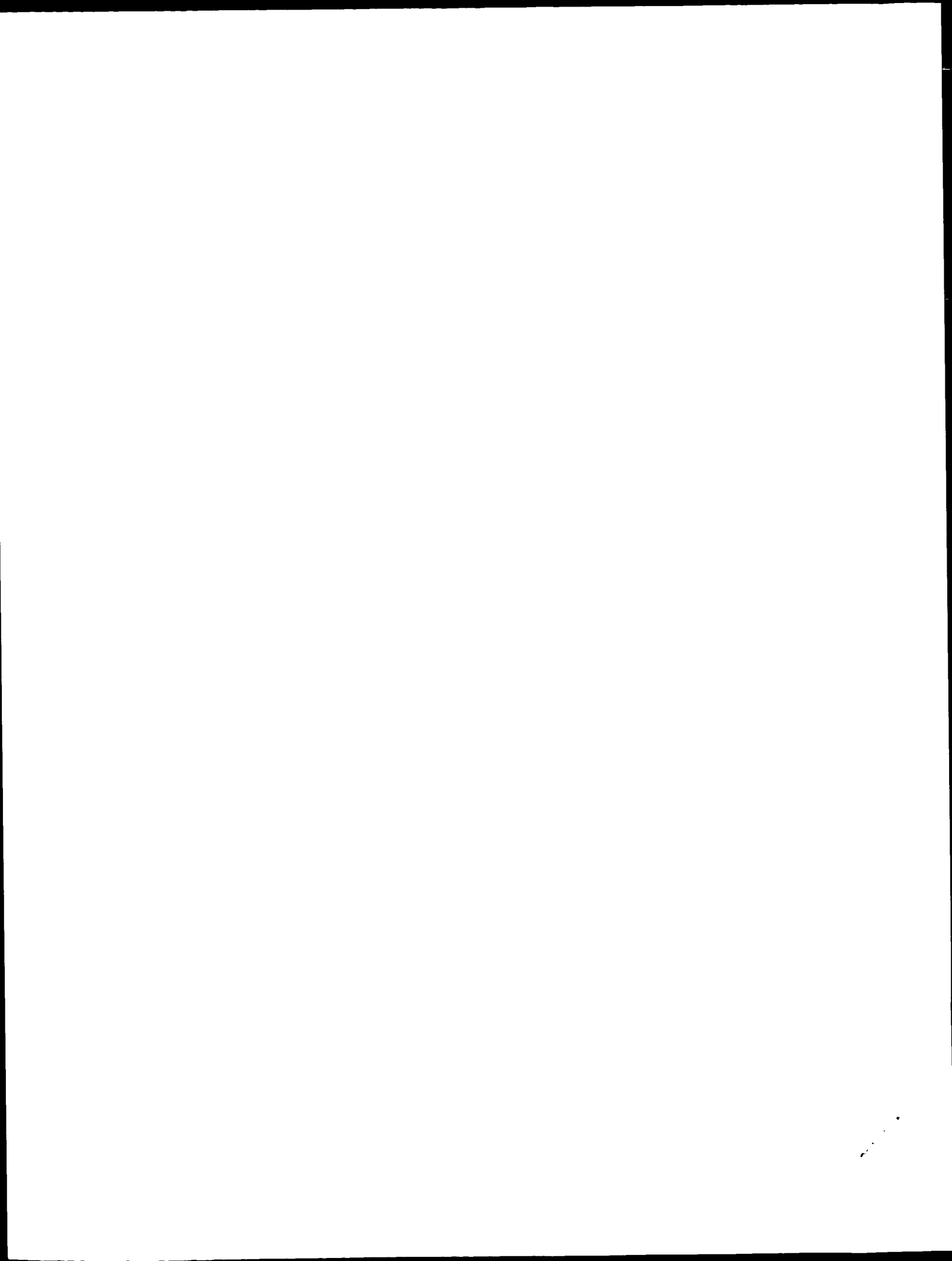
 RESULT 15
 Q9LQK5
 ID Q9LQK5 PRELIMINARY; PRT; 20 AA.
 AC Q9LQK5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Transcription factor AP1 (Fragment).
 OS Citrus sinensis (Sweet orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=2711;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu C., Xu C., Lin B.;
 RT "Molecular cloning of APETALA1 (AP1) gene from orange (Citrus
 RT sinensis).";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF263991; AAF74291.1; -
 FT NON_TER 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2493 MW; 3F1D0C6F8F5C1EA5 CRC64;

 Query Match 26.7%; Score 28; DB 10; Length 20;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 Qy 3 LSQETFSDLWK 13
 Db 9 LTHESISDLQK 19

Search completed: February 12, 2003, 11:14:59
 Job time : 38.2083 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:11:31 ; Search time 10.2917 Seconds
(without alignments)
76.572 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDLMKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.5	27.1	24	1 Y3KD NEUCR	P22702 neurospora
2	27	25.7	20	1 LECB_IRIHO	P36231 iris hollan
3	26	24.8	20	1 CRIC_SPIOL	P30806 spinacia ol
4	24	22.9	10	1 HTF_HELZE	P16353 heliothis z
5	24	22.9	20	1 CP35_PAPSP	P80056 papio sp. (
6	24	22.9	23	1 TL17_SPIOL	P81778 spinacia ol
7	24	22.9	23	1 XYC1_ACIGB	P46365 acinetobact
8	23	21.9	10	1 AKHX_LOCM1	P81626 locusta mig
9	22.5	21.4	25	1 LPCT_YEAST	P08521 saccharomyc
10	22	21.0	13	1 NP1_LYMST	P80178 lymnaea sta
11	22	21.0	13	1 NP2_LYMST	P80179 lymnaea sta
12	22	21.0	13	1 NP4_LYMST	P80181 lymnaea sta
13	22	21.0	13	1 NP5_LYMST	P80182 lymnaea sta
14	22	21.0	16	1 IBA4_PIG	P24854 sus scrofa
15	22	21.0	24	1 DMS6_PHYBI	P21490 phyllomedus
16	21.5	20.5	12	1 UR2_SCVCA	P35490 scyllorhinu
17	21	20.0	8	1 HTF2_PERAM	P04549 periplaneta
18	21	20.0	10	1 HTF2_CARMO	P11385 carausius m
19	21	20.0	15	1 URE1_MORMO	P17337 morganella
20	21	20.0	17	1 AC16_SOYEN	P15986 glycine max
21	21	20.0	18	1 CPAX_BOVIN	P22779 bos taurus
22	21	20.0	21	1 NDK_CANAL	P04595 tabanus atr
23	20	19.0	8	1 AKH_TABAT	P04548 periplaneta
24	20	19.0	8	1 HTF1_PERAM	P04548 periplaneta
25	20	19.0	10	1 HTF_TABAT	P80180 lymnaea sta
26	20	19.0	13	1 NP3_LYMST	P82697 periplaneta
27	20	19.0	17	1 PH4_PERAM	P82419 pachycondyl
28	20	19.0	18	1 PCG6_PACGO	P81217 equus cabal
29	20	19.0	19	1 AL22_HORSE	P12666 cavia porce
30	20	19.0	19	1 IRBP_CAVPO	P82420 pachycondyl
31	20	19.0	19	1 PCG7_PACGO	P13193 zea mays (m
32	20	19.0	20	1 PSF7_MAIZE	P56239 litoria cae
33	20	19.0	22	1 CR32_LITCE	

34 20 19.0 22 1 CR33_LITCE P56240 litoria cae
35 20 19.0 23 1 IRBP2_PIG P24853 sus scrofa
36 20 19.0 23 1 IRBP_RABIT P12664 oryctolagus
37 20 19.0 23 1 UDP_LACCA P19662 lactobacill
38 20 19.0 25 1 FLAA_TREPH P21983 treponema p
39 20 19.0 25 1 PCW1_PACGO P82423 pachycondyl
40 20 19.0 25 1 PCW2_PACGO P82424 pachycondyl
41 19 18.1 8 1 AKHG_GRYBI P14086 gryllus bim
42 19 18.1 8 1 CLP_THICU P80498 thiobacillu
43 19 18.1 8 1 HTF_TENMO P25419 tenebrio mo
44 19 18.1 10 1 HTF_NAUCI P10939 nauphoeta c
45 19 18.1 10 1 URA7_HUMAN P34990 homo sapien

ALIGNMENTS

RESULT 1
Y3KD_NEUCR
ID Y3KD_NEUCR STANDARD; PRT; 24 AA.
AC P22702;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 2.8 kDa protein in ARG-2 5'region.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90293033; PubMed=2141606;
RA Orbach M.J., Sachs M.S., Yanofsky C.;
RT "The Neurospora crassa arg-2 locus. Structure and expression of the
RT gene encoding the small subunit of arginine-specific carbamoyl
RT phosphate synthetase."
RL J. Biol. Chem. 265:10981-10987(1990).
CC -!- FUNCTION: MAY HAVE A REGULATOR ROLE IN THE PRODUCTION OF
CC ARGININE-SPECIFIC CARBAMOYL PHOSPHATE SYNTHETASE.
CC -!- SIMILARITY: TO YEAST CPAI LEADER PEPTIDE (AC P08521).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J05512; AAA33610.1; -.
DR PIR; B42224; B42224.
KW Hypothetical protein.
SQ SEQUENCE 24 AA; 2779 MW; 8FF33F527EAD244C CRC64;
Query Match 27.1%; Score 28.5; DB 1; Length 24;
Best Local Similarity 53.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 4 SQETFS-DLWKLL 15
||: ||: ||:
Db 10 SQDYLSDHLWRL 22
RESULT 2
LECB_IRIHO
ID LECB_IRIHO STANDARD; PRT; 20 AA.
AC P36231;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-
DE binding lectin subunit B) (Fragment).
OS Iris hollandica (Dutch iris).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
 OC Iris.
 OX NCBI_TaxID=35876;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. GOLDEN HARVEST, and CV. PROF. BLAAUW; TISSUE=Bulb;
 RX MEDLINE=94171801; PubMed=8125993;
 RA Mo H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;
 RT "Isolation and characterization of an
 RT N-acetyl-D-galactosamine-binding lectin from Dutch Iris bulbs which
 RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal).";
 RL J. Biol. Chem. 269:7656-7673(1994).
 CC -1- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE
 CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES
 CC IRRESPECTIVE OF BLOOD GROUP TYPE.
 CC -1- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.
 KW Lectin.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;
 Query Match 25.7%; Score 27; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PLSOET 7 25.7% | | | | |
 DB 6 PLSOET 11 | | | | |
 RESULT 3
 CRIC SPOL STANDARD; PRT; 20 AA.
 ID _CRIC SPOL STANDARD; PRT; 20 AA.
 AC P3086;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=93176159; PubMed=8439313;
 RA Menegazzi P., Guzzo F., Baldan B., Mariani P., Treves S.;
 RT "Purification of calreticulin-like protein(s) from spinach leaves.";
 RL Biochem. Biophys. Res. Commun. 190:1130-1135(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR PIR; PC1241; PC1241.
 DR PIR; PC1240; PC1240.
 DR InterPro; IPR001580; Calreticulin.
 DR PROSITE; PS00803; CALRETICULIN 1; PARTIAL.
 DR PROSITE; PS00804; CALRETICULIN 2; PARTIAL.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding; Glycoprotein.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2645 MW; 00FAB4C9DEEDCB0F CRC64;
 Query Match 24.8%; Score 26; DB 1; Length 20;
 Best Local Similarity 44.4%; Pred. No. 5.5e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 QETFSDLWK 13 24.8% | | | | |
 DB 6 EERFEGWE 13 | | | | |

RESULT 4
 HTF HELZE
 ID _HTF HELZE STANDARD; PRT; 10 AA.
 AC P16353;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrichalosaemic hormone (Hez-HRTH).
 OS Heliothis zea (Corn earworm) (Bollworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
 OX NCBI_TaxID=7113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=88326324; PubMed=3415690;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
 RA Tseng C.M., Zhang Y.S., Hayes D.K.;
 RT "Isolation and primary structure of a neuropeptide hormone from
 RT Heliothis zea with hypertrichalosemic and adipokinetic activities.";
 RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
 CC -1- FUNCTION: HYPERTRICHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A31571; A31571.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;
 Query Match 22.9%; Score 24; DB 1; Length 10;
 Best Local Similarity 62.5%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 QETFSDLW 12 22.9% | | | | |
 DB 1 QLTFSGW 8 | | | | |
 RESULT 5
 CP35_PAPSP
 ID _CP35_PAPSP STANDARD; PRT; 20 AA.
 AC P80056;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYFIIAS) (P450 FA) (6-beta-
 DE testosterone hydroxylase) (Fragment).
 OS Papio sp. (Baboon).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Papio.
 OX NCBI_TaxID=61183;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=92174920; PubMed=1541278;
 RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
 RT "Purification of two cytochrome P450 isozymes related to CYP2A and
 RT CYP3A gene families from monkey (baboon, Papio papio) liver
 RT microsomes. Cross reactivity with human forms.";
 RL Eur. J. Biochem. 204:641-648(1992).
 CC -1- FUNCTION: 6-BETA-TESTOSTERONE HYDROXYLASE.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- INDUCTION: BY PHENOBARBITAL.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR; S21176; S21176.

DR InterPro; IPR001128; Cytochrome P450.
 DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2226 MW; 3FEF8B6B62BC0F36 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 20;
 Best Local Similarity 46.7%; Pred. No. 1.1e+03;
 Matches 7; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 1 PPLSQTFSDLWKL 15
 | | | | |
 Db 5 PDLAVET---WLL 15

RESULT 6
 TL17_SPIOL
 ID TL17_SPIOL STANDARD; PRT; 23 AA.
 AC P81778;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 17.4 kDa protein (P17.4) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE AND REVISIONS TO 13 AND 15.
 RA Schubert M., Peterson U., Funk C., Schroeder W.P., Kieselbach T.;
 RT "The chloroplast lumen from Arabidopsis thaliana";
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 RN [2]
 RP SEQUENCE OF 1-16.
 RC TISSUE=Leaf;
 RX MEDLINE=98175931; PubMed=9506969;
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
 RT "The thylakoid lumen of chloroplasts - isolation and
 characterization.";
 RL J. Biol. Chem. 273:6710-6716 (1998).
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KW Chloroplast; Thylakoid.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2571 MW; 022C92717AE9AF2D CRC64;

Query Match 22.9%; Score 24; DB 1; Length 23;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQE 6
 | | | | |
 Db 6 PPLSND 11

RESULT 7
 XYC1_ACIGB
 ID XYC1_ACIGB STANDARD; PRT; 23 AA.
 AC P46365;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Benzaldehyde dehydrogenase [NAD+] I (EC 1.2.1.28) (Fragment).
 OS Acinetobacter genomosp. 11.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=106649;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 11171 / NCIB 8250 / CIP 63.46 / B94;
 RX MEDLINE=91113163; PubMed=1989592;
 RA Chalmers R.M., Keen J.N., Fewson C.A.;

RT "Comparison of benzyl alcohol dehydrogenases and benzaldehyde
 RT dehydrogenases from the benzyl alcohol and mandelate pathways in
 RT Acinetobacter calcoaceticus and from the TOL-plasmid-encoded toluene
 RT pathway in Pseudomonas putida. N-terminal amino acid sequences, amino
 RT acid compositions and immunological cross-reactions.";
 RL Biochem. J. 273:99-107 (1991).
 CC -1- CATALYTIC ACTIVITY: Benzaldehyde + NAD(+) + H(2)O = benzoate +
 CC NADH.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; PARTIAL.
 DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; PARTIAL.
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2750 MW; 50496D4930DF9E40 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 23;
 Best Local Similarity 23.1%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 PPLSQTFSDLWK 13
 | | | | |
 Db 1 PNQTKIIIEQWK 13

RESULT 8
 AKHX_LOCMI
 ID AKHX_LOCMI STANDARD; PRT; 10 AA.
 AC P81626;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptide hormone.
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RA Siegest K.J.;
 RL Submitted (DEC-1998) to the SWISS-PROT data bank.
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
 CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
 CC -1- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 10 10 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 62.5%; Pred. No. 7.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLW 12
 | | | | |
 Db 1 QVTFSDRW 8

RESULT 9
 LPCP_YEAST
 ID LPCP_YEAST STANDARD; PRT; 25 AA.
 AC P08521;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE CPA1 leader peptide.
 GN YOR302W.
 OS Saccharomyces cerevisiae (Baker's yeast).

Accession	Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
<p> RX MEDLINE=93238777; PubMed=8477756; RA Johnsen A.H., Rehfeld J.F.; RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail, RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in RT invertebrates?"; RRL Eur. J. Biochem. 213:875-879(1993). CCC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY. DR PIR; S32471; S32471. FT Neuropeptide; Amidation. KW MOD_RES 13 13 SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64; </p>	21.0%;	Score 22; DB 1; Length 13;	50.0%;	Pred. No. 1.4e+03;	1; Mismatches 3; Indels 0; Gaps 0;		
<p> QY 3 LSQETFSFD 10 : DB 5 ISSSAFSD 12 </p>							
<p> RESULT 11 NP2_LYMST ID NP2_LYMST STANDARD; PRT; 13 AA. AC P80179; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DT 01-JUL-1993 (Rel. 26, Last annotation update) DE Lymnaea-DP-amide 2. OS Lymnaea stagnalis (Great pond snail). OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora; OC Lymnaeidae; Lymnaea. OX NCBI_taxID=6523; RN [1] RP RC TISSUE=Ganglion; MEDLINE=93238777; PubMed=8477756; RA Johnsen A.H., Rehfeld J.F.; RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail, RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in RT invertebrates?"; RRL Eur. J. Biochem. 213:875-879(1993). CCC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY. DR PIR; S32472; S32472. FT Neuropeptide; Amidation. KW MOD_RES 13 13 SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5A5A5 CRC64; </p>	21.0%;	Score 22; DB 1; Length 13;	50.0%;	Pred. No. 1.4e+03;	1; Mismatches 3; Indels 0; Gaps 0;		
<p> QY 3 LSQETFSFD 10 : DB 5 ISSSAFSD 12 </p>							
<p> RESULT 12 NP4_LYMST ID NP4_LYMST STANDARD; PRT; 13 AA. AC P80181; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DT 01-JUL-1993 (Rel. 26, Last annotation update) DE Lymnaea-DP-amide 4. OS Lymnaea stagnalis (Great pond snail). OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora; OC Lymnaeidae; Lymnaea. OX NCBI_taxID=6523; RN [1] RP RC TISSUE=Ganglion; MEDLINE=93238777; PubMed=8477756; RA Johnsen A.H., Rehfeld J.F.; RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail, RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in RT invertebrates?"; RRL Eur. J. Biochem. 213:875-879(1993). CCC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY. DR PIR; S32472; S32472. FT Neuropeptide; Amidation. KW MOD_RES 13 13 SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5A5A5 CRC64; </p>	21.0%;	Score 22; DB 1; Length 13;	50.0%;	Pred. No. 1.4e+03;	1; Mismatches 3; Indels 0; Gaps 0;		
<p> QY 3 LSQETFSFD 10 : DB 5 ISSSAFSD 12 </p>							

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RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnaeaFamides, a new family of neuropeptides from the pond snail,
RL Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETFSFSD 10
   :|:|:|
Db 5 ISNSAFSD 12

RESULT 13
NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymna-DP-amide 5.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93238777; PubMed=8477756;
RX Johnsen A.H., Rehfeld J.F.;
RT "LymnaeFamides, a new family of neuropeptides from the pond snail,
RL Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -|- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETFSFSD 10
   :|:|:|
Db 5 ISSAFSD 12

RESULT 14
IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA MEDLINE=92109718; PubMed=1722398;

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RA Coleman M.E., Pan Y.-C.E., Esherton T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -|- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac.pr.
DR InterPro; IPR000716; Thyroglobulin 1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQE 6
   ||:|:|
Db 7 PPPSEE 12

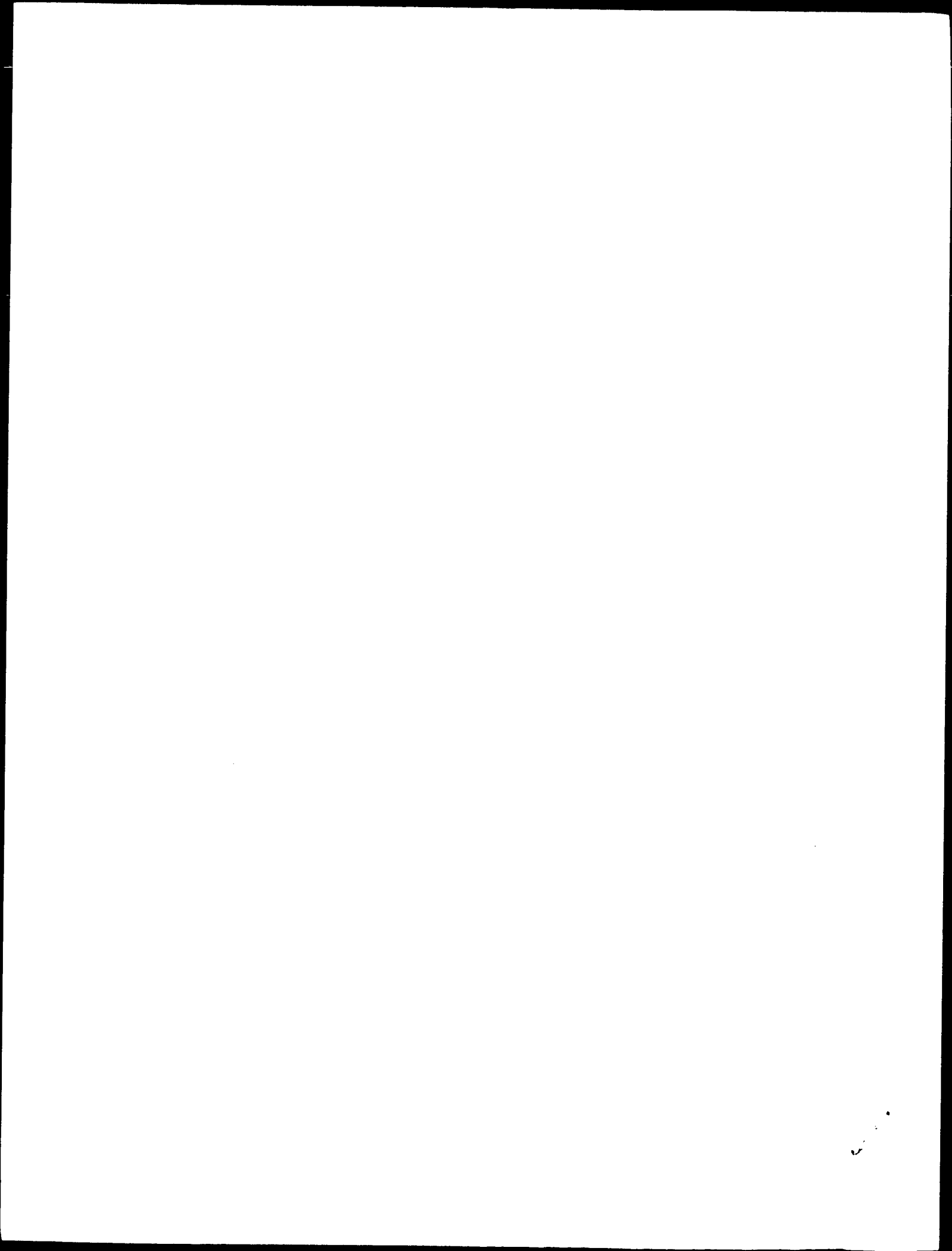
RESULT 15
DMS6_PHYBI STANDARD; PRT; 24 AA.
ID DMS6_PHYBI
AC P81490;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dermaseptin BVI (Dermaseptin B6).
OS Phyllomedusa bicolor (Two-colored leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8393;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=98278974; PubMed=9614066;
RA Charpentier S., Amiche M., Mester J., Vouille V., Le Caer J.-P.,
RA Nicolas P., Delfour A.;
RT "Structure, synthesis, and molecular cloning of dermaseptins B, a
RT family of skin peptide antibiotics.";
RL J. Biol. Chem. 273:14690-14697(1998).
CC -|- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY
CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE DERMASEPTIN FAMILY.
KW Antibiotic; Multigene family; Amphibian skin; Amidation.
FT MOD_RES 24 24 AMIDATION (POTENTIAL).
SQ SEQUENCE 24 AA; 2665 MW; E5987D7F50E08F4F CRC64;

Query Match 21.0%; Score 22; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 LWKLLPEN 18
   |||:|:|
Db 2 LWKDILKN 9

```

Search completed: February 12, 2003, 11:14:05
 Job time : 10.2917 secs



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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:22 ; Search time 20.5833 Seconds
(without alignments)
88.739 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQFTFSDLWKLPPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	32.4	19	2	B61409
2	33	31.4	24	2	I50387
3	30	28.6	24	2	T42442
4	28.5	27.1	24	2	B42224
5	27	25.7	23	2	D25865
6	26	24.8	18	2	A59396
7	26	24.8	20	2	D42842
8	26	24.8	20	2	PC1240
9	26	24.8	20	2	A61506
10	26	24.8	20	2	PH1334
11	26	24.8	23	2	PH1334
12	25	23.8	14	2	A35105
13	25	23.8	15	2	PA0110
14	25	23.8	20	2	A60372
15	25	23.8	20	2	A53592
16	25	23.8	25	2	A34921
17	24.5	23.3	20	2	PH1336
18	24	22.9	10	2	A31571
19	24	22.9	11	2	S41747
20	24	22.9	20	2	S21176
21	24	22.9	20	2	PC2347
22	24	22.9	20	2	JN0252
23	24	22.9	22	2	F23734
24	24	22.9	23	2	S13238
25	24	22.9	23	2	T42259
26	24	22.9	25	2	B53415
27	23.5	22.4	24	2	S35641
28	23	21.9	8	2	S11545
29	23	21.9	9	2	A24244

30 23 21.9 15 2 S20410 protein kinase (EC
31 23 21.9 23 2 S65379 cytochrome-c oxida
32 23 21.9 24 2 T42257 phosphoprotein pho
33 22.5 21.4 25 2 S25434 gene CPA1 leader p
34 22 21.0 5 2 S70615 endo-1,4-beta-xyla
35 22 21.0 8 2 S16324 hypothetical prote
36 22 21.0 13 2 S32471 lymnaDFamide 1 - g
37 22 21.0 13 2 S32472 lymnaDFamide 2 - g
38 22 21.0 13 2 S32474 lymnaDFamide 4 - g
39 22 21.0 13 2 S32475 lymnaDFamide 5 - g
40 22 21.0 14 2 B44854 L-2,4-diaminobuty
41 22 21.0 16 2 JH0517 insulin-like growt
42 22 21.0 17 2 S59481 hydroxyproline-ric
43 22 21.0 20 2 A60812 plasma proteinase
44 22 21.0 20 2 A56894 intracrySTALLINE c
45 22 21.0 21 2 S68023 nucleoside-diphosp

ALIGNMENTS

RESULT 1

B61409 genome polyprotein (clone L3/S2) - Skalica virus (fragment)
C;Species: Skalica virus

C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Nov-2000
C;Accession: B61409

R;Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.
J. Gen. Virol. 72, 333-338, 1991

A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by mon
A;Reference number: A61409; MUID:91132129; PMID:1847173

A;Accession: B61409

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: genomic RNA

A;Residues: 1-19 <GUI>

C;Superfamily: yellow fever virus genome polyprotein

Query Match 32.4%; Score 34; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 81;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQFTFSDLW 12

Db 2 PPVYRTGTDCW 13

RESULT 2

I50387 c-myc protein - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50387

R;Westaway, D.; Payne, G.; Varmus, H.E.

Proc. Natl. Acad. Sci. U.S.A. 81, 843-847, 1984

A;Title: Proviral deletions and oncogene base-substitutions in insertional mutagenized

A;Reference number: I50387; MUID:84144799; PMID:632173

A;Accession: I50387

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-24 <WES>

A;Cross-references: GB:K01440; NID:g212357; PIDN:AAA48964.1; PID:g212358

Query Match 31.4%; Score 33; DB 2; Length 24;

Best Local Similarity 47.4%; Pred. No. 1.5e+02;

Matches 9; Conservative 1; Mismatches 3; Indels 6; Gaps 2;

QY 1 PPLSQFTFSDLWK--LLP 16

Db 2 PPAPSE--DIWKKFELLP 17

RESULT 3

T42442

protein phosphatase - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
 C:Accession: T42442
 R:Zeke, T.; Gergely, P.; Dombradi, V.
 A:Submitted to: The EMBL Data Library, July 1996
 A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis elegans

A:Reference number: Z22025
 A:Accession: T42442
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <ZEK>
 A:Cross-references: EMBL:Z77728; PIDN:CAE01287.1
 C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match 28.6%; Score 30; DB 2; Length 24;
 Best Local Similarity 58.3%; Pred. No. 4.2e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 FSDLWKLPPENG 19
 :||| |||
 Db 2 YSLLALLELNG 13

RESULT 4
 B42224
 hypothetical protein (arg-2 5' region) - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 21-Jul-2000
 C:Accession: B42224
 R:Orbach, M.J.; Sachs, M.S.; Yanofsky, C.
 J. Biol. Chem. 265, 10981-10987, 1990
 A:Title: The Neurospora crassa arg-2 locus. Structure and expression of the gene encoding the arginine deiminase
 A:Reference number: A42224; MUID:90293033; PMID:2141606
 A:Accession: B42224
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-24 <ORB>
 A:Cross-references: GB:J05512; NID:g168864; PIDN:AAA33610.1; PID:g168866

Query Match 27.1%; Score 28.5; DB 2; Length 24;
 Best Local Similarity 53.8%; Pred. No. 7.1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 4 SQETPSD-LWKL 15
 :||| |||
 Db 10 SQYLSDLWRL 22

RESULT 5
 D25865
 gamma-crystallin IV - common carp (fragment)
 C:Species: Cyprinus carpio (common carp)
 C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 21-Nov-1997
 C:Accession: D25865
 R:Chou, S.H.; Chen, S.W.; Lo, T.B.
 FEBS Lett. 209, 107-110, 1986
 A:Title: The amino-terminal sequences of four major carp gamma-crystallin polypeptides
 A:Reference number: A91369; MUID:87105907; PMID:3803569
 A:Accession: D25865
 A:Molecule type: protein
 A:Residues: 1-23 <CHI>
 A:Note: the residues 3-ile, 15-Asn, 17-Asp, 18-Cys, and 20-His were also found
 C:Superfamily: beta-crystallin
 C:Keywords: duplication

Query Match 25.7%; Score 27; DB 2; Length 23;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LSQETPSD 10
 :||| |||
 Db 14 LSYETWSD 21

RESULT 6

A59396

Tha P 1 - Thaumetopoea pityocampa (fragment)
 C:Species: Thaumetopoea pityocampa
 C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 03-Jun-2002
 C:Accession: A59396
 R:Moneo, I.

submitted to the Protein Sequence Database, September 2001
 A:Description: Isolation and characterization of a major allergen of the pine processionary moth
 A:Reference number: A59396
 A:Accession: A59396
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <MON>
 A:Experimental source: I5
 A:Note: IGB-binding protein, major allergen

Query Match 24.8%; Score 26; DB 2; Length 18;
 Best Local Similarity 38.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 6 ETFSDLWKLPPEN 18
 :||| :
 Db 2 ETYSKXDTIDVN 14

RESULT 7

A60728

Cytochrome P450 3A, troleanomycin-induced - sheep (fragment)
 N:Contains: oxidoreductase (EC 1.-.-.-)
 C:Species: Ovis sp. (sheep)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-Mar-1999
 C:Accession: A60728
 R:Pineau, T.; Galtier, P.; Bonfils, C.; Derancourt, J.; Maurel, P.
 Biochem. Pharmacol. 39, 901-909, 1990
 A:Title: Purification of a sheep liver cytochrome P-450 from the P450I11A gene subfamily
 A:Reference number: A60728; MUID:90179800; PMID:2310415

A:Accession: A60728
 A:Molecule type: protein
 A:Residues: 1-20 <PIN>
 A:Comment: This cytochrome P450 isozyme is a member of the P450I11A family but is not found in sheep
 C:Genetics:
 A:Gene: CYP3A
 C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C:Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 24.8%; Score 26; DB 2; Length 20;
 Best Local Similarity 46.7%; Pred. No. 1.4e+03;
 Matches 7; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

Qy 1 PPLSQETPSDLWKL 15
 :||| :
 Db 5 PSFSKET----WVLL 15

RESULT 8

D42842

antifungal 2S storage albumin large chain - radish (fragment)
 C:Species: Raphanus sativus (radish)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C:Accession: D42842
 R:Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden, J. Biol. Chem. 267, 15301-15309, 1992
 A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus sativus)
 A:Reference number: A42842; MUID:92348373; PMID:1633977

A:Accession: D42842
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <TER>
 A:Experimental source: seed
 A:Note: sequence extracted from NCBI backbone (NCBI:109925)

C;Superfamily: wheat alpha-amylase inhibitor

Query Match 24.8%; Score 26; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 PPLSQETFSDL 11
||| | : :
Db 8 PPLQQCCNNL 18

RESULT 9

PC1240

calcium-binding protein, 53K - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Aug-1997
C;Accession: PC1240; PC1241
R;Menegazzi, P.; Guzzo, F.; Balzan, B.; Mariani, P.; Treves, S.
Biochem. Biophys. Res. Commun. 190, 1130-1135, 1993
A;Title: Purification of calreticulin-like protein(s) from spinach leaves.
A;Reference number: PC1240; MUID:93176159; PMID:8439313
A;Accession: PC1240
A;Molecule type: protein
A;Residues: 1-20 <MEN>
A;Experimental source: leaf
A;Note: 53K form
A;Accession: PC1241
A;Molecule type: protein
A;Residues: 1-20 <ME2>
A;Experimental source: leaf
A;Note: 55K form
C;Superfamily: calreticulin
C;Keywords: calcium binding; metal binding

Query Match 24.8%; Score 26; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETFSDLWK 13
: | | | :
Db 5 EERFEDGWE 13

RESULT 10

alpha-1-antitrypsin - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C;Accession: A61506
R;Amemiya, S.; Yamamoto, K.; Sinohara, H.
Comp. Biochem. Physiol. B 100, 293-296, 1991
A;Title: Purification, characterization, and acute phase response of plasma alpha-1-antitrypsin from golden hamster.
A;Reference number: A61506; MUID:92191572; PMID:1724745
A;Accession: A61506
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <AME>

Query Match 24.8%; Score 26; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 4 SQETFSDLWK 13
: | | | :
Db 3 AQET--DAWK 10

RESULT 11

PHI334
Ig heavy chain DJ region (clone C280-120) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI334

R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma.
A;Reference number: PHI302; MUID:93094761; PMID:1460419
A;Accession: PHI334

A;Molecule type: DNA
A;Residues: 1-23 <WAS>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 24.8%; Score 26; DB 2; Length 23;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLW 12
||| | : | :
Db 8 PPVYVYVMDVM 19

RESULT 12

A35105
hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35105
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in Neurospora crassa.
A;Reference number: A35105; MUID:90263093; PMID:2160856

A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-14 <SAV>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 23.8%; Score 25; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 SDLWKLLPENG 19
||| | : | :
Db 2 SFLWTLQLKG 12

RESULT 13

PA0110
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 26-Apr-1996
C;Accession: PA0110
R;Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A;Reference number: PA0109
A;Accession: PA0110
A;Molecule type: protein
A;Residues: 1-15 <KAW>

Query Match 23.8%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TFSDL 11
||| | : | :
Db 3 TFSDL 7

RESULT 14

A60372
pollen allergen Poa-pi - Kentucky bluegrass (fragment)
C;Species: Poa pratensis (Kentucky bluegrass)

C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 09-Jun-2000
C;Accession: A60372; A33086
R;Ekramoddoullah, A.K.M.
Int. Arch. Allergy Appl. Immunol. 93, 371-377, 1990
A;Title: Two-dimensional gel electrophoretic analyses of Kentucky bluegrass and rye grass
ence of Poa p I allergen.
A;Reference number: A60372; MUID:91317571; PMID:2101126
A;Accession: A60372
A;Molecule type: protein
A;Residues: 1-20

C;Superfamily: expansin
C;Keywords: hydroxyproline; pollen
F;5,8/Modified site: hydroxyproline (Pro) #status experimental

Query Match 23.8%; Score 25; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PLSQETFSDLW 12
| : |
Db 8 PXITATYGDKW 18

RESULT 15
A53592
H+-exporting ATPase (EC 3.6.3.6) 24k chain - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 03-Jun-2002
C;Accession: A53592
R;Yokoyama, K.; Akabane, Y.; Ishii, N.; Yoshida, M.
J. Biol. Chem. 269, 12248-12253, 1994
A;Title: Isolation of prokaryotic V-OV-1-ATPase from a thermophilic eubacterium Thermus
A;Reference number: A53592; MUID:94216345; PMID:8163530
A;Accession: A53592
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <YOK>
C;Keywords: hydrolase

Query Match 23.8%; Score 25; DB 2; Length 20;
Best Local Similarity 46.2%; Pred. No. 2e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSQETFSDLWKLL 15
| | | : |
Db 7 LSQEVETIQALL 19

Search completed: February 12, 2003, 11:15:31
Job time : 21.5933 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:43:13 ; Search time 30 Seconds
(without alignments)
18.635 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFTSLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 127244

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.ppep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	85.7	19	4	US-09-081-975-13
2	77	73.3	15	1	US-08-277-660A-1
3	77	73.3	15	1	US-08-277-660A-4
4	77	73.3	15	1	US-08-424-957-1
5	77	73.3	15	1	US-08-424-957-20
6	77	73.3	15	4	US-09-035-686-1
7	77	73.3	15	4	US-09-035-686-20
8	74	70.5	15	1	US-08-277-660A-5
9	74	70.5	15	1	US-08-424-957-21
10	74	70.5	15	4	US-09-035-686-21
11	74	70.5	16	4	US-09-081-975-23
12	65	61.9	15	3	US-09-280-047-6
13	65	61.9	15	4	US-08-208-573B-6
14	65	61.9	15	5	PCT-US95-02856-6
15	60	57.1	18	4	US-09-081-975-22
16	59	56.2	11	1	US-08-277-660A-9
17	59	56.2	11	1	US-08-424-957-17
18	59	56.2	11	4	US-09-035-686-17
19	59	56.2	13	4	US-09-236-415-5
20	57	54.3	11	1	US-08-424-957-45
21	57	54.3	11	1	US-08-424-957-46
22	57	54.3	11	4	US-09-035-686-45
23	57	54.3	11	4	US-09-035-686-46
24	57	54.3	14	4	US-09-400-653A-7
25	57	54.3	14	4	US-09-248-061B-7
26	56	53.3	11	1	US-08-277-660A-10
27	56	53.3	11	1	US-08-277-660A-15

28 56 53.3 11 1 US-08-424-957-23 Sequence 23, Appl
29 56 53.3 11 1 US-08-424-957-28 Sequence 28, Appl
30 56 53.3 11 1 US-08-424-957-40 Sequence 40, Appl
31 56 53.3 11 4 US-09-035-686-23 Sequence 23, Appl
32 56 53.3 11 4 US-09-035-686-28 Sequence 28, Appl
33 56 53.3 11 4 US-09-035-686-40 Sequence 40, Appl
34 55 52.4 10 1 US-08-277-660A-7 Sequence 7, Appl
35 55 52.4 10 1 US-08-424-957-11 Sequence 11, Appl
36 55 52.4 10 4 US-09-035-686-11 Sequence 11, Appl
37 55 52.4 11 1 US-08-277-660A-20 Sequence 20, Appl
38 55 52.4 11 1 US-08-424-957-33 Sequence 33, Appl
39 55 52.4 11 1 US-08-424-957-34 Sequence 34, Appl
40 55 52.4 11 1 US-08-424-957-35 Sequence 35, Appl
41 55 52.4 11 1 US-08-424-957-36 Sequence 36, Appl
42 55 52.4 11 1 US-08-424-957-42 Sequence 42, Appl
43 55 52.4 11 4 US-09-035-686-33 Sequence 33, Appl
44 55 52.4 11 4 US-09-035-686-34 Sequence 34, Appl
45 55 52.4 11 4 US-09-035-686-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-081-975-13
; Sequence 13, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-081-975-13

Query Match 85.7%; Score 90; DB 4; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.2e-08;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 PPLSQETFSDLWLKLPEN 18
    |||||:|||||
Db 1 PPLSQETFSDLWLKLPEN 18
    |||||:|||||

RESULT 2
US-08-277-660A-1
; Sequence 1, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-4

Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWLK 14
    |||||
Db 2 PPLSQETFSDLWLK 15
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RESULT 4
US-08-424-957-1
; Sequence 1, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

QY 5 QETFSDLWLKLPEN 18
    |||||
Db 1 QETFSDLWLKLPEN 14
    |||||

RESULT 3
US-08-277-660A-4
; Sequence 4, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187

Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWLKLPEN 18
    |||||
Db 1 QETFSDLWLKLPEN 14
    |||||
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;
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-1

Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFSDLWLKLLPEN 18
Db 1 QETFSDLWLKLLPEN 14

RESULT 5

US-08-424-957-20
Sequence 20, Application US/08424957
Patent No. 5770377

;
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-20

Query Match 73.3%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLK 14
Db 2 PPLSQETFSDLWLK 15

RESULT 6

US-09-035-686-1
Sequence 1, Application US/09035686
Patent No. 6153391

;
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-1

Query Match 73.3%; Score 77; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QETFSDLWLKLLPEN 18
Db 1 QETFSDLWLKLLPEN 14

RESULT 7

US-09-035-686-20
Sequence 20, Application US/09035686
Patent No. 6153391

;
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS


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; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-21

Query Match 70.5%; Score 74; DB 4; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWLKP 16
Db 1 PLSQETFSGLWLKP 15

RESULT 11
US-09-081-975-23
; Sequence 23, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-081-975-23

Query Match 70.5%; Score 74; DB 4; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.2e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWLKP 17
Db 1 PLSQETFDLWSLLPD 16

RESULT 12
US-09-280-047-6
; Sequence 6, Application US/09280047
; Patent No. 6068462
; GENERAL INFORMATION:
; APPLICANT: GOUJELI, SAID A.
; TITLE OF INVENTION: QUANTITATION OF INDIVIDUAL PROTEIN
; TITLE OF INVENTION: KINASE ACTIVITY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: One South Pinckney Street, P.O. Box 2599
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53701-2599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/280,047
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,573
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SARA, CHARLES S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-5353
; TELEFAX: (608) 257-9175
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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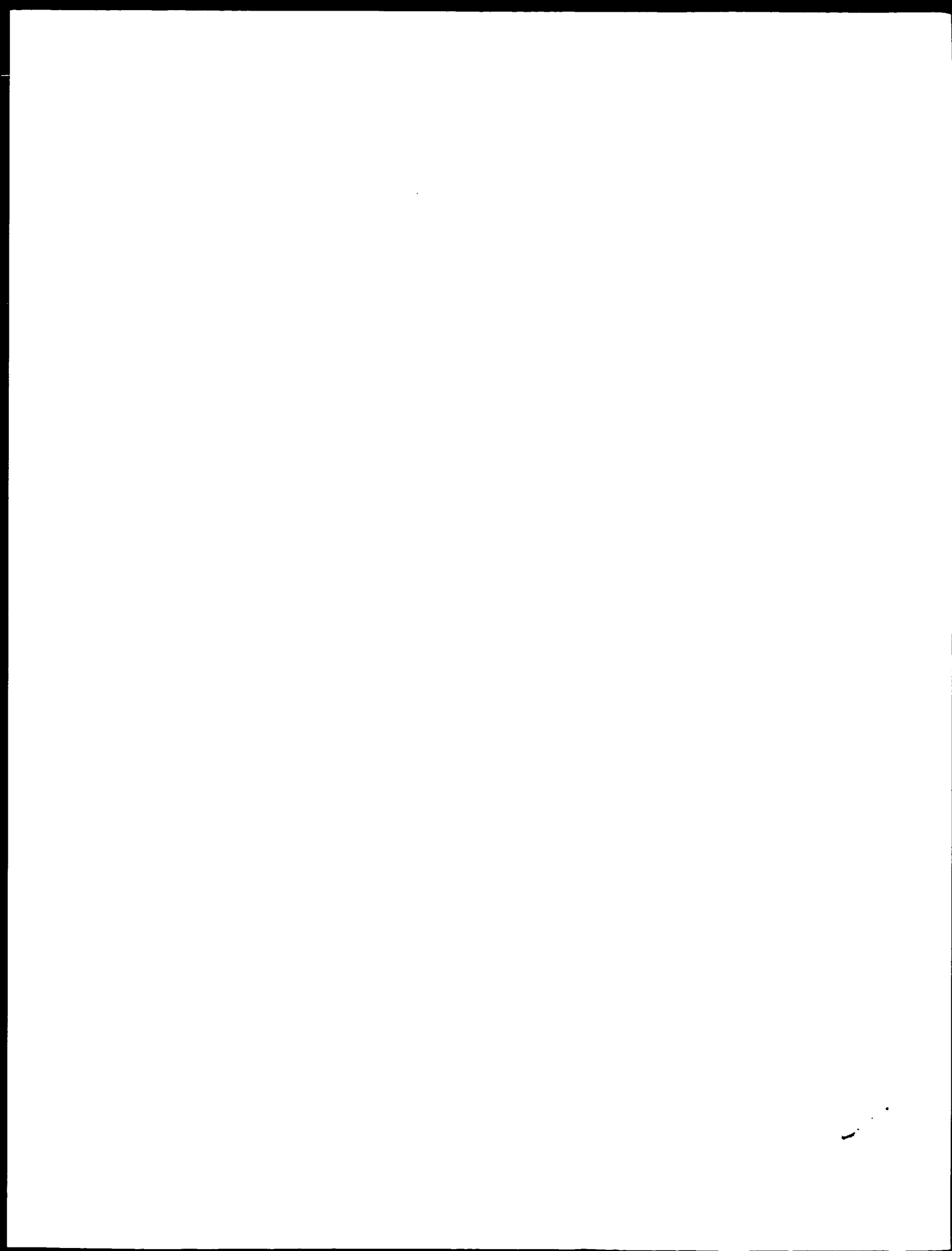


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; TELE:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; US-09-081-975-22

Query Match      57.1%; Score 60; DB 4; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.0024;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  2 PLSQETFSDLWKL 14
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Db  3 PLSQESFEDLWKM 15
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Search completed: February 12, 2003, 10:46:27
Job time : 30 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:44:28 ; Search time 56 Seconds
(without alignments)
28.428 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 152190

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA New.*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	87.6	19	7	US-60-438-805-9
2	81	77.1	15	6	US-10-211-088-141
3	70	66.7	13	5	US-09-701-080C-22
4	70	66.7	13	5	US-09-701-080C-27
5	59	56.2	11	5	US-09-189-702A-286
6	41	39.0	14	6	US-10-049-428-6
7	40	38.1	7	5	US-09-701-080C-12
8	35	33.3	14	6	US-10-049-428-7
9	31.5	30.0	14	6	US-10-268-332-53
10	31.5	30.0	16	6	US-10-225-567A-1177
11	31	29.5	9	5	US-09-189-702A-7
12	31	29.5	12	5	US-09-281-717A-31
13	31	29.5	12	5	US-09-281-717A-33
14	31	29.5	12	5	US-09-281-717A-35
15	31	29.5	12	5	US-09-830-693B-6
16	31	29.5	12	5	US-09-830-693B-8
17	30	28.6	16	6	US-10-348-131-49
18	29	27.6	15	6	US-10-169-026-3
19	29	27.6	16	6	US-10-225-567A-942
20	29	27.6	17	1	PCT-US02-28371-70
21	29	27.6	17	6	US-10-236-878-70
22	29	27.6	18	5	US-09-552-802B-30
23	28.5	27.1	18	5	US-09-632-036E-11
24	28	26.7	7	6	US-10-174-717A-36
25	28	26.7	16	7	US-60-427-045-297
26	28	26.7	18	6	US-10-283-599-219

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27 26.7 18 6 US-10-232-410-9 Sequence 9, Appli
28 25.7 9 5 US-09-641-528-25751 Sequence 25751, A
29 25.7 9 5 US-09-641-528-29042 Sequence 29042, A
30 25.7 9 5 US-09-641-528-25751 Sequence 25751, A
31 25.7 9 5 US-09-641-528A-29042 Sequence 29042, A
32 25.7 9 6 US-10-029-206A-67 Sequence 67, Appl
33 25.7 9 6 US-10-301-644-18 Sequence 18, Appl
34 25.7 9 6 US-10-028-075B-67 Sequence 67, Appl
35 25.7 10 5 US-09-641-528-463 Sequence 463, App
36 25.7 10 5 US-09-641-528-1442 Sequence 1442, Ap
37 25.7 10 5 US-09-641-528-12880 Sequence 12880, A
38 25.7 10 5 US-09-641-528-15661 Sequence 15661, A
39 25.7 10 5 US-09-641-528-25791 Sequence 25791, A
40 25.7 10 5 US-09-641-528-29085 Sequence 29085, A
41 25.7 10 5 US-09-641-528A-463 Sequence 463, App
42 25.7 10 5 US-09-641-528A-1442 Sequence 1442, Ap
43 25.7 10 5 US-09-641-528A-12880 Sequence 12880, A
44 25.7 10 5 US-09-641-528A-15661 Sequence 15661, A
45 25.7 10 5 US-09-641-528A-25791 Sequence 25791, A

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ALIGNMENTS

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RESULT 1
US-60-438-805-9
; Sequence 9, Application US/60438805
; GENERAL INFORMATION:
; APPLICANT: KODADEK, THOMAS
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS
; FILE REFERENCE: UTSD:935USP1
; CURRENT APPLICATION NUMBER: US/60/438,805
; CURRENT FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-60-438-805-9

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Query Match 87.6%; Score 92; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLPEN 18
Db 1 PLSQETFSDLWKLLPEN 17
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|||||

RESULT 2
US-10-211-088-141
; Sequence 141, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT

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Query Match 66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;

Query Match	39.0%	Score 41;	DB 6;	Length 14;
Best Local Similarity	69.2%	Pred. No. 4.3;		
Matches	9;	Conservative	1; Mismatches	3; Indels
				0; Gaps
Qy	1	PPLSQETTFSDLWK	13	
Db	2	PPLSQEAFALLKK	14	

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RESULT 7
US-09-701-080C-12
; Sequence 12, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from p53
US-09-701-080C-12
Query Match      38.1%; Score 40; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 FSDLWKL 14
Db 1 FSDLWKL 7
|||||

RESULT 8
US-10-049-428-7
; Sequence 7, Application US/10049428
; GENERAL INFORMATION:
; APPLICANT: Charles, Ian G.
; APPLICANT: Xu, Weiming
; APPLICANT: Liu, Lizhi
; TITLE OF INVENTION: Undruggable Screen for Drug Discovery
; FILE REFERENCE: HO-P02380US0
; CURRENT APPLICATION NUMBER: US/10/049,428
; CURRENT FILING DATE: 2000-07-28
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: GB 9918077
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutagen
US-10-049-428-7
Query Match      33.3%; Score 35; DB 6; Length 14;
Best Local Similarity 53.8%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;
QY 1 PLSQTFSDLWK 13
Db 2 PLSQAFALLKK 14
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RESULT 9
US-10-268-332-53
; Sequence 53, Application US/10268332
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP6MY3, EXPRESSED HIGHLY
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; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-53
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Query Match      30.0%; Score 31.5; DB 6; Length 14;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 6 BTFSDELWK 13
Db 5 BTFSDELWK 13
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RESULT 10
US-10-225-567A-1177
; Sequence 1177, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1177
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1177
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Query Match      30.0%; Score 31.5; DB 6; Length 16;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 3; Gaps 1;
QY 4 SOETFSDELWKLPEN 18
Db 5 SQENHNS---RILPEN 16
|||||
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RESULT 11
US-09-189-702A-7
; Sequence 7, Application US/09189702A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Kast, W. Martin
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune, Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 39963-20019.20
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; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.24V9 peptide 1323.02
US-09-189-702A-7

Query Match      29.5%; Score 31; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KLLPEN 18
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Db 1 KLLPEN 6

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RESULT 12
US-09-281-717A-31
; Sequence 31, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MUTAGEN
; LOCATION: (5)..(5)
; OTHER INFORMATION: Leu --> Arg (L454R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (7)..(7)
; OTHER INFORMATION: Leu --> Arg (L456R)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (8)..(8)
; OTHER INFORMATION: Glu --> Lys (E457K)
US-09-281-717A-31

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10
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Db 3 PPLFLEVFE 12

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RESULT 13
US-09-281-717A-33

```

```

; Sequence 33, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-33

```

```

Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 1 PPLSQETFS 10
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Db 3 PPLFLEVFE 12

```

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RESULT 14
US-09-281-717A-35
; Sequence 35, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-281-717A-35

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Query Match      29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PPLSQETFS 10
   ||| | | |
Db 3 PPLFLEVFE 12

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RESULT 15
US-09-830-693B-6
; Sequence 6, Application US/09830693B

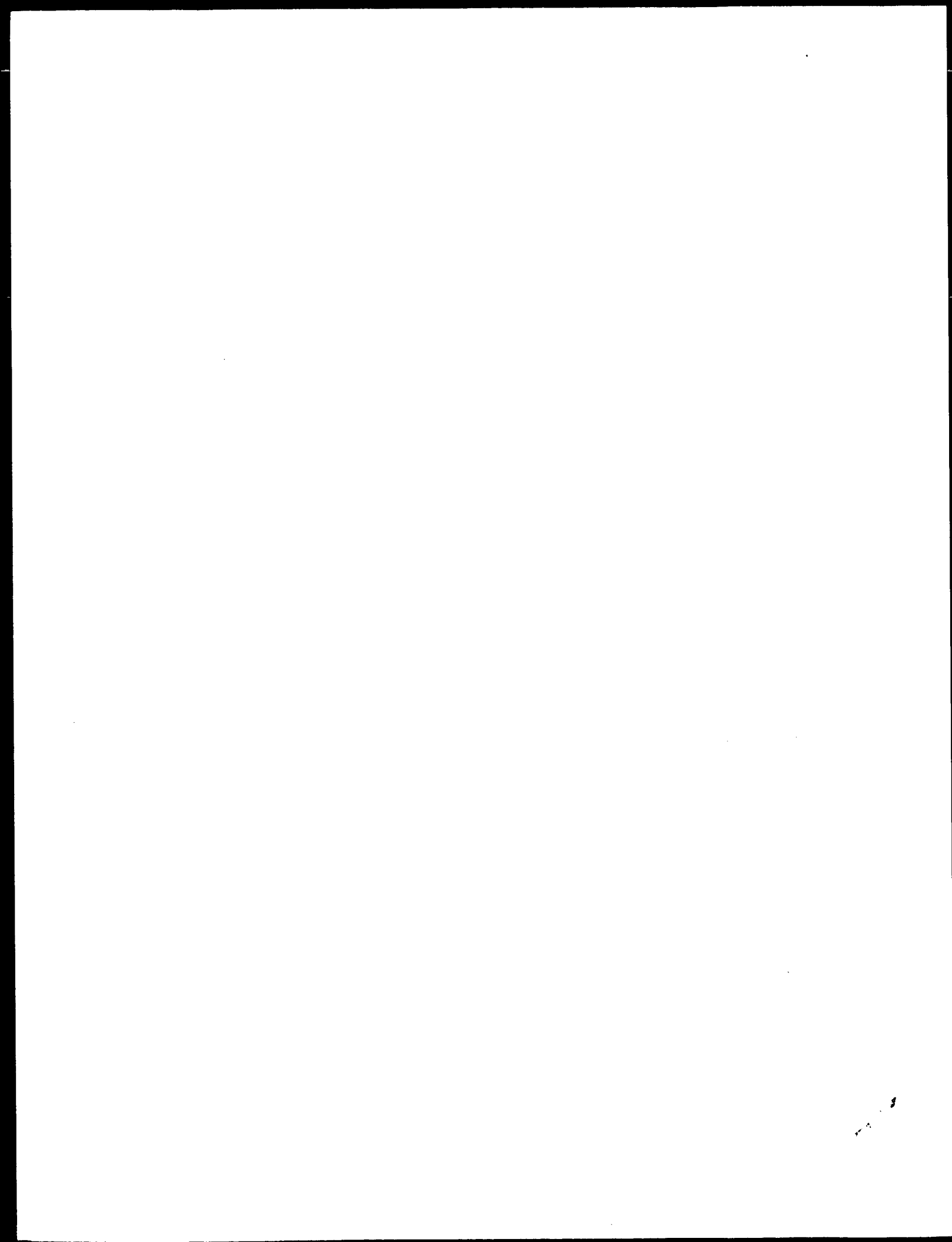
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GENERAL INFORMATION:
; APPLICANT: Shiau, Andrew
; APPLICANT: Kushner, Peter
; APPLICANT: Agard, David
; APPLICANT: Greene, Geoffrey
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 9811-013-999
; CURRENT APPLICATION NUMBER: US/09/830,693B
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/US99/06937
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US 60/113,014
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-693B-6

Query Match 29.5%; Score 31; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQTFSD 10
| | | | |
Db 3 PPLFLEVFD 12

Search completed: February 12, 2003, 10:49:50
Job time : 56 secs



GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:45:03 ; Search time 11 Seconds
(without alignments)
44.130 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPEN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 36726

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubpaa/US08 NEW PUB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/ECT NEW PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06 NEW PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09 NEW PUB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US10_NEW PUB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US60_NEW PUB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	18	10	US-09-214-371-74
2	92	87.6	19	10	US-09-732-384-7
3	90	85.7	19	12	US-10-155-059-13
4	89	84.8	19	10	US-09-214-371-1
5	77	73.3	15	10	US-09-732-384-5
6	74	70.5	16	12	US-10-155-059-23
7	66	62.9	12	10	US-09-214-371-17
8	65	61.9	15	10	US-09-950-692-6
9	60	57.1	18	12	US-10-155-059-22
10	59	56.2	16	10	US-09-214-371-39
11	57	54.3	14	9	US-10-024-123-7
12	55	52.4	12	10	US-09-214-371-7
13	54	51.4	12	10	US-09-214-371-24
14	54	51.4	16	10	US-09-214-371-41
15	53	50.5	16	10	US-09-214-371-40
16	49	46.7	12	10	US-09-214-371-25
17	49	46.7	12	10	US-09-214-371-26
18	48	45.7	14	10	US-09-214-371-33
19	48	45.7	14	10	US-09-214-371-34

Sequence 17, Appl
Sequence 3, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 24, Appl
Sequence 83, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 110, Appl
Sequence 13, Appl
Sequence 22, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 52, Appl
Sequence 69, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 35, Appl
Sequence 18, Appl
Sequence 5, Appl

US-10-155-059-17
US-09-019-679-3
US-10-155-059-21
US-09-214-371-20
US-10-155-059-24
US-09-214-371-83
US-09-732-384-4
US-10-155-059-1
US-09-214-371-37
US-09-214-371-38
US-09-214-371-35
US-09-214-371-36
US-10-155-059-2
US-09-840-277-66
US-09-920-552-110
US-09-214-371-13
US-09-214-371-22
US-09-214-371-46
US-09-214-371-47
US-09-214-371-52
US-09-840-277-69
US-09-281-717-31
US-09-281-717-33
US-09-281-717-35
US-10-024-123-18
US-09-732-384-5

ALIGNMENTS

RESULT 1
US-09-214-371-74
; Sequence 74, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picketsley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the interaction of P53 and MDM2
; FILE REFERENCE: 4-209377A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5,5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2
US-09-732-384-7
; Sequence 7, Application US/09732384
; Patent No. US20020132977A1

```
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jijie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
; US-09-732-384-7

Query Match      87.6%; Score 92; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PLSQETFSDLWKLLPEN 18
Db      1 PLSQETFSDLWKLLPEN 17

RESULT 3
US-10-155-059-13
; Sequence 13, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-155-059-13

Query Match      85.7%; Score 90; DB 12; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 PPLSQETFSDLWKLLPEN 18
Db      1 PPLSQETFSDLWKLLPEN 18

RESULT 4
US-09-214-371-1
; Sequence 1, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; US-09-214-371-1

Query Match      84.8%; Score 89; DB 10; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PLSQETFSDLWKLLPEN 18
Db      1 PLSQETFSDLWKLLPEN 17

RESULT 5
US-09-732-384-6
; Sequence 6, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; APPLICANT: Gu, Jijie
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
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; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-6

Query Match      73.3%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLPEN 18
Db 1 QETFSDLWKLLPEN 14

RESULT 6
US-10-155-059-23
; Sequence 23, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155.059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-155-059-23

Query Match      70.5%; Score 74; DB 12; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.8e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPE 17
Db 1 PLSQETFSDLWKLLPD 16

RESULT 7
US-09-214-371-17
; Sequence 17, Application US/09214371B
```

```
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17

Query Match      62.9%; Score 66; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QETFSDLWKLLP 16
Db 1 QETFSDLWKLLP 12

RESULT 8
US-09-950-692-6
; Sequence 6, Application US/09950692
; Patent No. US20020106701A1
; GENERAL INFORMATION:
; APPLICANT: Goueli, Said A
; TITLE OF INVENTION: Quantitation of Individual Protein Kinase Activity
; FILE REFERENCE: kinase
; CURRENT APPLICATION NUMBER: US/09/950,692
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 08/208,573
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-950-692-6

Query Match      61.9%; Score 65; DB 10; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0006;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWK 13
Db 2 PPLSQEAFADLWK 14

RESULT 9
US-10-155-059-22
; Sequence 22, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
```

;
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-155-059-22

Query Match 57.1%; Score 60; DB 12; Length 18;
Best Local Similarity 76.9%; Pred. No. 0.0041;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PLSQETFSDLWK 14
| | | | | | | | | |
Db 3 PLSQSFEDLWKM 15

RESULT 10
US-09-214-371-39
; Sequence 39, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picklesley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 39
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Biotin-Ser
; NAME/KEY: VARIANT
; LOCATION: (16)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-39

Query Match 56.2%; Score 59; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 QETFSDLWKLL 15
| | | | | | | | | |
Db 5 QETFSDLWKLL 15

RESULT 11
US-10-024-123-7
; Sequence 7, Application US/10024123
; Publication No. US20030022263A1
; GENERAL INFORMATION:
; APPLICANT: Kastan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and
; FILE REFERENCE: 2427/1f142
; CURRENT APPLICATION NUMBER: US/10/024,123
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/400,653
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-123-7

Query Match 54.3%; Score 57; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPLSQETFSDL 11
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Db 4 PPLSQETFSDL 14

RESULT 12
US-09-214-371-7
; Sequence 7, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picklesley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2

```
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-7

Query Match 52.4%; Score 55; DB 10; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 5 QETFSDLWKLLP 16
Db 1 QPTFSDYWKLLP 12

RESULT 13
US-09-214-371-24
Sequence 24, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Ac-Gln
NAME/KEY: VARIANT
LOCATION: (12)
OTHER INFORMATION: X = Pro-NH2
OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-24

Query Match 51.4%; Score 54; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ETFSDLWKLL 15
Db 2 ETFSDLWKLL 11

RESULT 14
US-09-214-371-41
Sequence 41, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Biotin-Ser
NAME/KEY: VARIANT
LOCATION: (16)
OTHER INFORMATION: X = Pro-NH2
US-09-214-371-41

APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Biotin-Ser
NAME/KEY: VARIANT
LOCATION: (16)
OTHER INFORMATION: X = Pro-NH2
US-09-214-371-41

Query Match 51.4%; Score 54; DB 10; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLL 15
Db 5 QETFSDYWKLL 15

RESULT 15
US-09-214-371-40
Sequence 40, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Biotin-Ser
NAME/KEY: VARIANT
LOCATION: (16)
OTHER INFORMATION: X = Pro-NH2
US-09-214-371-40
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Query Match 50.5%; Score 53; DB 10; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 QETFSDLWKLL 15
| | | | | | | | | |
Db 5 QPTFSDLWKLL 15

Search completed: February 12, 2003, 10:50:08
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:36:07 ; Search time 34 Seconds
(without alignments)
74.464 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 278369

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /SID82/gcgdata/geneseq/geneseq-embl/AA1989.DAT:*
11: /SID82/gcgdata/geneseq/geneseq-embl/AA1990.DAT:*
12: /SID82/gcgdata/geneseq/geneseq-embl/AA1991.DAT:*
13: /SID82/gcgdata/geneseq/geneseq-embl/AA1992.DAT:*
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20: /SID82/gcgdata/geneseq/geneseq-embl/AA1999.DAT:*
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22: /SID82/gcgdata/geneseq/geneseq-embl/AA2001.DAT:*
23: /SID82/gcgdata/geneseq/geneseq-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	97	92.4	19	AAW47074	p53/RB interaction
5	81	77.1	15	AA106310	Human p53 peptide
6	77	73.3	15	AAR54909	Immunodominant epi
7	77	73.3	15	AAR54910	Immunodominant epi
8	77	73.3	15	AAR5914	p53 protein bindin
9	77	73.3	15	AAR59157	Peptide #1. Unide
10	77	73.3	15	AAG89500	p53 DR 3a motif bi

11	77	73.3	15	22	AAG89730	p53 DR3 binding pe
12	77	73.3	17	20	AAV45227	Peptide 9-25.
13	74	70.5	15	21	AAW29159	Peptide #3. Unide
14	74	70.5	15	21	AAW29163	Peptide #7. Unide
15	73	69.5	14	23	ABW5528	Biotinylated pepi
16	73	69.5	15	21	AAW29167	Peptide #11. Unid
17	71	67.6	15	21	AAW29161	Peptide #4. Unide
18	71	67.6	15	21	AAW29161	Peptide #5. Unide
19	70	66.7	13	21	AAV57799	HLA class II bindi
20	70	66.7	13	21	AAV57799	TRAM-interaction m
21	69	65.7	15	21	AAW29162	Peptide #6. Unide
22	69	65.7	15	21	AAW29164	Peptide #8. Unide
23	66.5	63.3	16	21	AAW29149	Ligand #1. Unide
24	66.5	63.3	16	21	AAW29158	Peptide #2. Unide
25	66	62.9	12	19	AAW37181	Human p53 wild-typ
26	66	62.9	12	19	AAW37188	Human oncogenic pr
27	66	62.9	12	21	AAW17075	Mdm/hdm antagonist
28	66	62.9	12	21	AAW17087	Mdm/hdm antagonist
29	66	62.9	12	23	ABW73170	Mdm/hdm antagonist
30	66	62.9	12	23	ABW73182	Mdm/hdm antagonist
31	66	62.9	16	19	AAW37201	Human oncogenic pr
32	65	61.9	15	16	AAW83012	Promega protein ki
33	65	61.9	15	21	AAW58559	Tumour suppressor
34	65	61.9	15	23	ABW9246	Target activatable
35	62	59.0	15	22	AAG89447	p53 DR supermotif
36	61	58.1	11	23	AAW52269	Miniature protein
37	61	58.1	12	19	AAW37190	Human oncogenic pr
38	61	58.1	12	21	AAW17077	Mdm/hdm antagonist
39	61	58.1	12	21	AAW17089	Mdm/hdm antagonist
40	61	58.1	12	23	ABW73172	Mdm/hdm antagonist
41	61	58.1	12	23	ABW73184	Mdm/hdm antagonist
42	61	58.1	16	19	AAW37203	Human oncogenic pr
43	60	57.1	12	19	AAW37189	Human oncogenic pr
44	60	57.1	12	21	AAW17076	Mdm/hdm antagonist
45	60	57.1	12	21	AAW17088	Mdm/hdm antagonist

ALIGNMENTS

RESULT 1

AAW82321
ID AAW82321 standard; Peptide; 19 AA.

XX AAW82321;

XX 22-FEB-1999 (first entry)

XX p53 homologue TIP peptide.

DE p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX Synthetic.

XX WO9847919-A1.

XX 29-OCT-1998.

XX 20-APR-1998; 98WO-GB01140.

XX 22-APR-1997; 97GB-0008089.

XX (UYDU-) UNIV DUNDEE.

XX Lane DP;

XX WPI; 1998-609975/51.

XX New substance with a mdm2 binding domain and coupling partner

XX Useful for stabilising in cells without an efficient mdm2-mediated

XX degradation pathway

XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds
 CC to mdm2. This peptide is used in the construction of a novel agent
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
 CC production of mdm2 in a population of cells. This agent is also used in
 CC the preparation of a therapeutic for activating p53, where the population
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53
 CC function. The agents for use in therapeutics for activating p53 can be
 CC used for the treatment of cancer, viral conditions or other conditions
 CC associated with non-functional p53.

XX Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPENG 19
 |||||
 Db 1 PPLSQETFSDLWKLLPENG 19

RESULT 2

AAW82319
 ID AAW82319 standard; Peptide; 19 AA.

XX AC AAW82319;

XX DT 22-FEB-1999 (first entry)

XX DE p53 homologue TIP peptide.

XX KW p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX OS Synthetic.

XX FN W09847525-A1.

XX PD 29-OCT-1998.

XX XX 20-APR-1998; 98WO-GB01144.

XX PR 22-APR-1997; 97GB-0008092.

XX XX (UYDU-) UNIV DUNDEE.

XX PI Lane DP;

XX DR WPI; 1998-609932/51.

XX New agents which inhibit interaction of p53 and mdm2 - useful for
 PT activating p53, e.g. for treating cancers, viral conditions or other
 PT conditions associated with non functional p53 or mdm2

PS Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds
 CC to mdm2. This peptide is used in the construction of a novel agent
 CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
 CC production of mdm2 in a population of cells. This agent is also used in
 CC the preparation of a therapeutic for activating p53, where the population
 CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
 CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
 CC reducing the clearance of p53 by mdm2, and can be used to activate p53
 CC function. The agents for use in therapeutics for activating p53 can be
 CC used for the treatment of cancer, viral conditions or other conditions
 CC associated with non-functional p53.

XX Sequence 19 AA;

Query Match • 100.0%; Score 105; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPENG 19
 |||||
 Db 1 PPLSQETFSDLWKLLPENG 19

RESULT 3

AAW37228
 ID AAW37228 standard; peptide; 18 AA.

XX AC AAW37228;

XX DT 20-JUL-1998 (first entry)

XX DE p53 N-terminal peptide fragment for Elisa TIP assay.

XX KW MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
 tumour; diagnosis; binding; viral infection; Elisa TIP assay.

XX OS Homo sapiens.

XX FN W09801467-A2.

XX PD 15-JAN-1998.

XX PF 04-JUL-1997; 97WO-EP03549.

XX PR 07-APR-1997; 97GB-0007041.

XX PR 05-JUL-1996; 96GB-0014197.

XX XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX PA (NOVS) NOVARTIS AG.

XX PI Boettger A, Boettger V, Chene P, Furet P, Garcia-echeverria C;

XX PI Hochkeppel H, Lane D, Picksley S;

XX DR WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with

PT p53 - useful in, e.g. diagnosis and treatment of cancer and viral

PT infections and identifying binding agents

PS Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP
 CC assay for analysing the interaction between human oncogenic protein MDM2
 CC and p53. The invention provides peptide derivatives capable of binding to
 CC the human MDM2. These peptides can specifically inhibit or block the
 CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting
 CC the interaction between the p53 and MDM2 can induce growth arrest or
 CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated
 CC levels of MDM2. The peptides may be used to identify molecules that bind
 CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They
 CC may also be used to purify binding partners especially MDM2, diagnose
 CC disease by measuring levels of MDM2 in blood of cancer and leukaemia
 CC patients and for treatment or prevention of disease involving p53/MDM2
 CC interactions, especially tumours and viral infections. The peptides can
 CC be administered nasally, rectally, orally or by injection. By interfering
 CC with MDM2/p53 interaction, the peptides can activate p53 function and
 CC accumulation in normal cells. The peptides which mimic the MDM2 binding
 CC site in p53, have a significantly greater blocking activity compared
 CC with wild-type p53.

XX Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

|||||

Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 4

AAW47074
ID AAW47074 standard; peptide; 19 AA.

AC AAW47074;
XX

DT 19-MAY-1998 (first entry)
XX

DE p53/Rb interaction inhibiting peptide 6 (residues 11-29 of human p53).
XX

KW Retinoblastoma gene; Rb; p53 protein; interaction; inhibitor;
KW tumour; apoptosis; modulator; medicine; veterinary; human.
XX

OS Synthetic.
OS Homo sapiens.
XX

XX WO9741433-A1.
XX

XX 06-NOV-1997.
XX

XX 29-APR-1997; 97WO-GB01168.
XX

XX 29-APR-1996; 96GB-0008937.
XX

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX

PI Kouzarides T;
XX

XX WPI; 1997-549887/50.
XX

PT Identifying compounds that modulate interaction of p53 and Rb
PT protein - or those that bind to Rb protein, used to induce
PT apoptosis, specifically for treatment of tumours
XX

PS Claim 36; Page 63; 83pp; English.
XX

CC This peptide fragment of p53 is an inhibitor of the interaction between
CC a p53 protein and a retinoblastoma (Rb) protein. This peptide
CC corresponds to residues 11-29 of human p53 (AAW47079). The interaction
CC between p53 and Rb is found to be critical for determining whether or not
CC a cell enters apoptosis. Apoptosis is prevented if interaction occurs.
CC The interaction is between regions 1-71 or 290-393 of p53 and region
CC 379-928 of Rb. The invention provides methods to identify compounds able
CC to modulate interaction or binding between p53 and Rb protein. The method
CC comprises combining p53 and Rb, or their fragments, with a test compound
CC and detecting interaction/binding between them. These inhibitory
CC compounds are used in human or veterinary medicine to modulate p53
CC activity and processes, specifically for inducing apoptosis in tumour
CC cells (possibly also in cells infected by virus), in vivo or in vitro.
CC Expression of these modulators by gene therapy methods is also
CC contemplated. Other activities that can be affected are transcription
CC repression, G1 arrest, DNA repair, homologous recombination and
CC 3'-5'-exonuclease activity. Modulation of interaction with Rb may also
CC stabilise p53.
XX

SQ Sequence 19 AA;

Query Match 92.4%; Score 97; DB 18; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.1e-08;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5

AAW06310
ID AAY06310 standard; Peptide; 15 AA.

XX

AC

XX AAY06310;

DT 06-SEP-1999 (first entry)

DE Human p53 peptide (aal3-27).

XX RB18A; p53 regulatory protein; apoptosis; neoplasia; inflammation;
KW wound healing; graft rejection; reperfusion injury;
KW myocardial infarction; stroke; traumatic brain injury;
KW neurodegenerative disease; ischaemia; toxemia; infection; AIDS;
KW hepatitis; breast cancer; ovarian cancer; colon cancer; diagnosis;
KW therapy; human.
XX

XX Homo sapiens.
XX

XX WO9931231-A1.
XX

XX 24-JUN-1999.
XX

XX 14-DEC-1998; 98WO-EP08560.
XX

XX 15-DEC-1997; 97EP-0403051.
XX

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX

XX Fraide R;
XX

XX WPI; 1999-395177/33.
XX

XX New p53 regulatory protein (RB18A) useful as, e.g. sources of probes
XX and primers to detect the transcription rate and abundance of RB18A
XX mRNA in lymphocytes
XX

XX Example 1; Page 25; 87pp; English.
XX

CC This synthetic peptide corresponds to amino acids 13-27 of human
CC p53. It was used to raise anti-peptide p53.1 and anti-RB18A
CC antibodies in rabbit. RB18A (see AAY06309) is a novel p53
CC regulatory protein of the invention. The antibodies were used in
CC immunoscreenings that led to the isolation of a cDNA clone (see
CC AX59124) encoding human RB18A. The invention provides methods and
CC compositions for the diagnostic and therapeutic applications of
CC RB18A, in particular for the diagnosis, prevention or treatment of
CC neoplasia.
XX

XX Sequence 15 AA;

Query Match 77.1%; Score 81; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLP 16

Db 1 PLSQETFSDLWKLLP 15

RESULT 6

AAR54909

ID AAR54909 standard; peptide; 15 AA.

XX AAR54909;
XX

DT 29-NOV-1994 (first entry)
XX

DE Immunodominant epitope from p53 N-terminal.
XX

XX cancer; pre-cancerous state; detection; diagnosis; human p53 gene;
KW immunodominant epitope; human cellular tumour antigen;
KW transformation-associated protein.
XX

XX Homo sapiens.
XX

XX WO9410306-A.
XX

RESULT 9
 AAB29157
 ID AAB29157 standard; Peptide; 15 AA.
 XX AC AAB29157;
 XX DT 02-FEB-2001 (first entry)
 XX DE Peptide #1.
 XX KW Fork head associated; FHA; domain; transcriptional control;
 XX KW DNA replication; DNA repair; cell cycle control.
 XX OS Unidentified.
 XX PN WO200057184-A2.
 XX PD 28-SEP-2000.
 XX PF 17-MAR-2000; 2000WO-GB01024.
 XX PR 19-MAR-1999; 99GB-0006432.
 XX PR 28-JUN-1999; 99GB-0015075.
 XX PA (KUDO-) KUDOS PHARM LTD.
 XX PI Jackson SP, Durocher D;
 XX PI WPI; 2000-664872/64.
 XX DR Assays and screening methods based on direct interaction between FHA
 PT domains and phosphopeptides, useful for characterizing binding and to
 PT identify binding partners and modulators of FHA domain-phosphopeptide
 PT binding.
 XX PS Disclosure; Fig 2; 92pp; English.
 XX CC The present invention relates to assays and screening methods based on
 CC a direct interaction between fork head associated (FHA) domains and
 CC phosphorylated polypeptides, for characterizing the binding of these
 CC molecules. FHA peptides may be useful for treating medical conditions
 CC associated with defects in transcriptional control, DNA replication,
 CC DNA repair, cell cycle control or other cellular process. The method
 CC may provide valuable insights into checkpoint signalling, has important
 CC implications for the functions of other FHA domain-containing
 CC proteins and provides basis for new lines of therapy. The present
 CC sequence is a peptide used in the present invention.
 XX SQ Sequence 15 AA;
 Query Match 73.3%; Score 77; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPLSQETFSDLWKL 14
 Db 1 PPLSQETFSDLWKL 15
 RESULT 10
 AAG89500
 ID AAG89500 standard; Peptide; 15 AA.
 XX AC AAG89500;
 XX DT 11-SEP-2001 (first entry)
 XX DE p53 DR 3a motif binding peptide exemplary sequence #3.
 XX KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;

KW vaccine; epitope; cytostatic.
 XX Homo sapiens.
 OS Synthetic.
 XX PN WO200141788-A1.
 XX PD 14-JUN-2001.
 XX PF 11-DEC-2000; 2000WO-US33629.
 XX PR 10-DEC-1999; 99US-0458297.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 XX WPI; 2001-381493/40.
 XX DR Epitope-based vaccines comprising p53 epitope having a specified
 PT sequences, useful for treating and preventing cancer, the epitopic
 PT peptides is useful as diagnostic agents and for evaluating immune
 PT response.
 XX PS Disclosure; Page 113; 138pp; English.
 XX CC The present invention describes isolated prepared p53 epitopes (I). Also
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a
 CC vaccine composition comprising (II), a unit dose of a peptide with less
 CC than 50 contiguous amino acids with 100% identity to the native peptide
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
 CC has cytostatic activity and can be used in vaccines. The vaccine
 CC composition is useful for treating or preventing cancer. (I) and (II)
 CC are useful as diagnostic agents and for evaluating immune responses.
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be
 CC present in whole antigens can be avoided with the use of the vaccine
 CC composition of (I). The ability to combine selected epitopes and
 CC further, to modify the composition of the epitopes enhances the
 CC immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigens, which might have their own
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
 CC represent amino acid sequences used in the exemplification of the
 CC present invention.
 XX SQ Sequence 15 AA;
 Query Match 73.3%; Score 77; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPLSQETFSDLWKL 14
 Db 2 PPLSQETFSDLWKL 15
 RESULT 11
 AAG89730
 ID AAG89730 standard; Peptide; 15 AA.
 XX AC AAG89730;
 XX DT 11-SEP-2001 (first entry)
 XX DE p53 DR3 binding peptide #1.
 XX KW Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
 KW vaccine; epitope; cytostatic.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX WO200141788-A1.
 PN 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US33629.
 PF 10-DEC-1999; 99US-0458297.
 XX (EPIM-) EPIMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 PI WPI; 2001-381493/40.
 DR Epitope-based vaccines comprising p53 epitope having a specified
 XX sequences, useful for treating and preventing cancer, the epitopic
 PT peptides is useful as diagnostic agents and for evaluating immune
 PT response -
 PS Example 5; Page 131; 138pp; English.
 XX The present invention describes isolated prepared p53 epitopes (I). Also
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising
 CC a vaccine composition comprising (II), a unit dose of a peptide with less
 CC than 50 contiguous amino acids with 100% identity to the native peptide
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
 CC has cytostatic activity and can be used in vaccines. The vaccine
 CC composition is useful for treating or preventing cancer. (I) and (II)
 CC are useful as diagnostic agents and for evaluating immune responses.
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be
 CC present in whole antigens can be avoided with the use of the vaccine
 CC composition of (I). The ability to combine selected epitopes and
 CC further, to modify the composition of the epitopes enhances the
 CC immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigens, which might have their own
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747
 CC represent amino acid sequences used in the exemplification of the
 CC present invention.
 XX Sequence 15 AA;
 SQ
 Query Match 73.3%; Score 77; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPLSQETFSDLWKL 14
 Db 2 PPLSQETFSDLWKL 15
 RESULT 12
 AAY45227
 ID AAY45227 standard; peptide; 17 AA.
 XX AAY45227;
 AC 06-JAN-2000 (first entry)
 DT p53 peptide 9-25.
 DE Immunisation; immunogenicity enhancer; rabies virus strain ERA;
 XX immunodominant T-helper cell determinant; nucleoprotein; antibody;
 KW post-translational modification; p53; cancer; diagnosis.
 KW Synthetic.
 OS
 XX

PN WO9946574-A2.
 XX 16-SEP-1999.
 XX 11-MAR-1999; 99WO-US04653.
 PF 11-MAR-1998; 98US-0077512.
 XX (WIST-) WISTAR INST.
 XX Otvos L, Ertl H, Thurin M, Hoffman R;
 PI WPI; 1999-561693/47.
 DR Methods of detecting post-translational modification level of p53,
 XX useful for diagnosis of cancer -
 PT Disclosure; Page 45; 59pp; English.
 PS The present invention describes a polypeptide comprising a portion of a
 CC p53 comprising a post-translationally modified amino acid residue where
 CC the modification is a phosphorylation, glycosylation or prenylation, and
 CC an immunogenicity enhancer. The polypeptide is used to detect anti-p53
 CC autoantibodies in a human patient. The antibody can be used to determine
 CC the post-translational modification state of a p53 protein. These are
 CC used especially in the diagnosis of cancer. The present sequence
 CC represents a p53 peptide used in the exemplification of the present
 CC invention.
 XX Sequence 17 AA;
 SQ
 Query Match 73.3%; Score 77; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PPLSQETFSDLWKL 14
 Db 4 PPLSQETFSDLWKL 17
 RESULT 13
 AAB29159
 ID AAB29159 standard; Peptide; 15 AA.
 XX AAB29159;
 AC 02-FEB-2001 (first entry)
 DT Peptide #3.
 DE Fork head associated; FHA; domain; transcriptional control;
 XX DNA replication; DNA repair; cell cycle control.
 KW Unidentified.
 XX WO200057184-A2.
 PN 28-SEP-2000.
 PD 17-MAR-2000; 2000WO-GB01024.
 PF 19-MAR-1999; 99GB-0006432.
 PR 28-JUN-1999; 99GB-0015075.
 XX (KUDO-) KUDOS PHARM LTD.
 XX Jackson SP, Durocher D;
 PI WPI; 2000-664872/64.
 DR Assays and screening methods based on direct interaction between FHA
 PT domains and phosphopeptides, useful for characterizing binding and to
 PT identify binding partners and modulators of FHA domain-phosphopeptide

```

PT binding -
XX
PS Disclosure; Fig 2; 92pp; English.
XX
CC The present invention relates to assays and screening methods based on
CC a direct interaction between fork head associated (FHA) domains and
CC phosphorylated polypeptides, for characterizing the binding of these
CC molecules. FHA peptides may be useful for treating medical conditions
CC associated with defects in transcriptional control, DNA replication,
CC DNA repair, cell cycle control or other cellular processes. The method
CC may provide valuable insights into checkpoint signalling, has important
CC implications for the functions of other FHA domain-containing
CC proteins and provides basis for new lines of therapy. The present
CC sequence is a peptide used in the present invention.
XX
SQ Sequence 15 AA;
  Query Match 70.5%; Score 74; DB 21; Length 15;
  Best Local Similarity 92.9%; Pred. No. 4.2e-05;
  Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
  |||:|||||
Db 2 PPLAQETFSDLWKL 15
  |||:|||||

RESULT 14
AAB29163
ID AAB29163 standard; Peptide; 15 AA.
XX
AC AAB29163;
XX
DT 02-FEB-2001 (first entry)
XX
DE Peptide #7.
XX
KW Fork head associated; FHA; domain; transcriptional control;
KW DNA replication; DNA repair; cell cycle control.
XX
OS Unidentified.
XX
PN WO200057184-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-GB01024.
XX
PR 19-MAR-1999; 99GB-0006432.
PR 28-JUN-1999; 99GB-0015075.
XX
PA (KUDO-) KUDOS PHARM LTD.
XX
PI Jackson SP, Durocher D;
XX
DR WPI; 2000-664872/64.
XX
PT Assays and screening methods based on direct interaction between FHA
PT domains and phosphopeptides, useful for characterizing binding and to
PT identify binding partners and modulators of FHA domain-phosphopeptide
PT binding -
XX
PS Disclosure; Fig 2; 92pp; English.
XX
CC The present invention relates to assays and screening methods based on
CC a direct interaction between fork head associated (FHA) domains and
CC phosphorylated polypeptides, for characterizing the binding of these
CC molecules. FHA peptides may be useful for treating medical conditions
CC associated with defects in transcriptional control, DNA replication,
CC DNA repair, cell cycle control or other cellular processes. The method
CC may provide valuable insights into checkpoint signalling, has important
CC implications for the functions of other FHA domain-containing
CC proteins and provides basis for new lines of therapy. The present
CC sequence is a peptide used in the present invention.
XX
SQ Sequence 15 AA;
  Query Match 70.5%; Score 74; DB 21; Length 15;
  Best Local Similarity 92.9%; Pred. No. 4.2e-05;
  Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKL 14
  |||:|||||
Db 2 PPLAQETFSDLWKL 15
  |||:|||||

RESULT 15
ABB05528
ID ABB05528 standard; Peptide; 14 AA.
XX
AC ABB05528;
XX
DT 22-APR-2002 (first entry)
XX
DE Biotinylated peptide SEQ ID NO:13.
XX
KW Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif;
KW CDP motif; cytostatic; nontropic; antiproliferative; cell proliferation;
KW growth; differentiation; cancer; neurodegenerative disorder;
KW spinal degeneration.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "phospho-Thr"
FT
XX
PN WO200183518-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-CA00632.
XX
PR 04-MAY-2000; 2000US-202166P.
PR 24-JAN-2001; 2001US-263774P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Nash P, Pawson T, Tang X, Tyers M;
XX
DR WPI; 2002-164074/21.
XX
PT New Cdc4 Phospho Design motif that targets molecules for ubiquitin
PT dependent proteolysis, is useful for the modulation of cell
PT proliferation i.e. cancer treatment -
XX
PS Example 2; Page 47; 83pp; English.
XX
CC The present invention describes a cdc4 phospho design (CPD) motif, (C),
CC that targets molecules for ubiquitin dependent proteolysis. (C) have
CC cytosolic, nontropic and antiproliferative activity. Also described is
CC a method for the treatment of a disease or condition where affected
CC cells have a defective protein, comprising administering (C) to promote
CC degradation of the target protein in cells by ubiquitin dependent
CC proteolysis. (C) can also be used for modulating the proliferation,
CC growth and/or differentiation of cells. (C) can be used to modulate
CC ubiquitin dependent proteolysis or cell proliferation, growth and or
CC differentiation of cells. (C) is useful in the treatment of cancers and
CC neurodegenerative disorders as well as spinal degeneration. The present
CC sequence represents a biotinylated peptide which is used in an example
CC from the present invention.
XX
SQ Sequence 14 AA;
  Query Match 69.5%; Score 73; DB 23; Length 14;
  Best Local Similarity 100.0%; Pred. No. 5.6e-05;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 1 PPLSQETFSDLWK 13
| | | | | | | | | |
Db 2 PPLSQETFSDLWK 14

Search completed: February 12, 2003, 10:43:48
Job time : 35 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:42:32 ; Search time 28 Seconds
(without alignments)
139.818 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 5270

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL 21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.5	19	5 P83003	P83003 entamoeba h
2	31	29.5	16	6 Q9BG58	Q9BG58 sox arane
3	30	28.6	14	6 Q77538	Q77538 bos taurus
4	29	27.6	17	8 Q9XNQ1	Q9XNQ1 boophilus m
5	27	25.7	11	4 Q9UELO	Q9UELO homo sapien
6	26	24.8	14	10 P82326	P82326 pisum sativ
7	26	24.8	17	11 Q9QVS7	Q9QVS7 mus sp. lac
8	26	24.8	18	4 Q9UJZ3	Q9UJZ3 homo sapien
9	25	23.8	16	12 Q83960	Q83960 influenzavi
10	25	23.8	17	2 Q9FOP3	Q9FOP3 paracoccus
11	25	23.8	18	6 P82674	P82674 bos taurus
12	25	23.8	18	12 Q84129	Q84129 influenzavi
13	25	23.8	19	10 Q22064	Q22064 dioscorea t
14	25	23.8	19	12 Q83965	Q83965 influenzavi
15	24	22.9	10	8 Q9MJQ5	Q9MJQ5 podospora c
16	24	22.9	10	11 Q9ESU5	Q9ESU5 mus musculus

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17 24 22.9 12 7 077919
18 24 22.9 14 8 Q9MJQ3
19 24 22.9 15 13 Q9PS10
20 24 22.9 16 12 Q83967
21 24 22.9 16 12 Q84055
22 24 22.9 17 11 Q9QVS6
23 23 21.9 8 11 Q9QV15
24 23 21.9 9 8 Q9TLM7
25 23 21.9 11 7 077895
26 23 21.9 11 7 077896
27 23 21.9 15 2 Q53580
28 23 21.9 15 4 Q9UEM3
29 23 21.9 15 4 Q9UC22
30 23 21.9 15 8 Q9T2K8
31 23 21.9 15 10 P83141
32 23 21.9 16 6 Q9TRD1
33 23 21.9 17 11 Q9QV58
34 23 21.9 17 12 Q69074
35 23 21.9 18 1 Q9UWJ7
36 23 21.9 19 4 Q9BVX6
37 23 21.9 19 11 Q9QV38
38 22 21.0 9 4 Q9S953
39 22 21.0 14 2 Q9RS18
40 22 21.0 17 15 Q72017
41 22 21.0 18 13 Q13167
42 21.5 20.5 19 6 Q19107
43 21 20.0 7 8 Q9S945
44 21 20.0 9 4 Q9H3Y3
45 21 20.0 13 11 Q91XP1

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ALIGNMENTS

RESULT 1

```

P83003
ID P83003 PRELIMINARY; PRT; 19 AA.
AC P83003;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Calreticulin-like protein (Fragment).
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE.
RC STRAIN=HM-1:IMMS;
RA Gonzalez E., Mendoza G., Ramos F., Garcia G., Moran P., Valadez A.,
RA Zaragoza M.E., Melendro E.I., Ximenez C.;
RT "Calreticulin-like molecule in trophozoites of Histolytica HM1-IMMS.";
RL Submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC -!- DEVELOPMENTAL STAGE: IN TROPHOZOITES.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON TER 19
SQ SEQUENCE 19 AA; 2488 MW; FC90BCAFEB1BA764 CRC64;

```

Query Match 30.5%; Score 32; DB 5; Length 19;

Best Local Similarity 45.5%; Pred. No. 2.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QETFSDLWKLL 15

Db 5 EETFENGWKXI 15

```

RESULT 2
Q9BG8      PRELIMINARY;      PRT;      16 AA.
AC
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE Thyroid hormone receptor alpha (Fragment).
GN THRA1.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin D., Serov O., Zhdanova N.;
RT "Mapping of five genes from human chromosome 17 to chromosome 1n of
RT the common shrew (Sorex araneus).";
RL Acta Theriol. (Warsz) 45:143-146(2000).
DR EMBL; AF314827; AAK13419.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 16 AA; 1951 MW; 7751863FE5F52E2 CRC64;

Query Match      29.5%; Score 31; DB 6; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQTFSD 10
   ||| |||
DB 4 PPLFLEVFED 13

RESULT 3
O77538     PRELIMINARY;      PRT;      14 AA.
AC
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED HOLSTEIN;
RX MEDLINE=99175163; PubMed=10075683;
RA Jiang H., Okamura C.S., Lucy M.C.;
RT "Isolation and characterization of a novel promoter for the bovine
RT growth hormone receptor gene.";
RL J. Biol. Chem. 274:7893-7900(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Identification of 5' untranslated variants of bovine growth hormone
RT receptor mRNA.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Jiang H., Lucy M.C.;
RT "Bovine GH receptor 5' UTR variants.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036297; AAC33315.2; -.

RESULT 4
Q9XN01     PRELIMINARY;      PRT;      17 AA.
AC
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
DE Cytochrome oxidase subunit 2 (Fragment).
GN COII.
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
RT Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110614; AAD28397.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 17 AA; 1988 MW; 319F2D4DA7DA11F3 CRC64;

Query Match      27.6%; Score 29; DB 8; Length 17;
Best Local Similarity 75.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SQTFSD 11
   ||| |||
DB 5 SQTTFSDM 12

RESULT 5
Q9UELO     PRELIMINARY;      PRT;      11 AA.
AC
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
DE FAS antigen (C95 antigen) (Fragment).
GN C95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISSUE=BL00D;
 RX MEDLINE=95355401; PubMed=7543095;
 RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
 RA Nakanishi Y.;
 RT "Transcription stimulation of the Fas-encoding gene by nuclear factor
 RT for interleukin-6 expression upon influenza virus infection.";
 RT J. Biol. Chem. 270:18007-18012(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
 RA Kuppers R., Rajewsky K.;
 RA "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
 RT cells.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
 RA "Somatic mutations of the CD95 gene in human B cells as a side-effect
 RT of the germinal center reaction.";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D31968; BAA20850.1; -;
 DR EMBL; AJ279011; CAC35539.1; -;
 DR EMBL; AJ279012; CAC35540.1; -;
 DR EMBL; AJ279013; CAC35541.1; -;
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;
 Query Match 25.7%; Score 27; DB 4; Length 11;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 11 LWKLLP 16
 Db 4 IWTLLP 9
 RESULT 6
 ID P82326 PRELIMINARY; PRT; 14 AA.
 AC P82326;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RP STRAIN=CV. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.
 KW Chloroplast; Thylakoid membrane.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;
 Query Match 24.8%; Score 26; DB 10; Length 14;
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PPLSQE 6
 Db 6 PPLSTE 11

RESULT 7
 Q9QVS7 PRELIMINARY; PRT; 17 AA.
 ID Q9QVS7;
 AC Q9QVS7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Lactate dehydrogenase-A (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95201434; PubMed=7534515;
 RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,
 RA Favor J.;
 RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
 RT mouse.";
 RL Mamm. Genome 5:777-780(1994).
 SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;
 Query Match 24.8%; Score 26; DB 11; Length 17;
 Best Local Similarity 30.8%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 Qy 1 PPLSOETFSDLWK 13
 Db 4 PELGTDAHKEQWK 16
 RESULT 8
 Q9UJZ3 PRELIMINARY; PRT; 18 AA.
 ID Q9UJZ3;
 AC Q9UJZ3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Oviduct glycoprotein (Fragment).
 GN OGP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee K.F., Kwok K.L., Agarwal A., Lee Y.L.;
 RT "Human oviduct glycoprotein promoter sequence";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF189710; AAF01085.1; -;
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2201 MW; 5E8FD91EA210E516 CRC64;
 Query Match 24.8%; Score 26; DB 4; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 LWKLL 15
 Db 1 MWKLL 5
 RESULT 9
 Q83960 PRELIMINARY; PRT; 16 AA.
 ID Q83960;
 AC Q83960;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Influenza A/ann arbor/6/60 (H2n2), non-structural protein (seg 8),
 DE cooh terminus of ns1 (Fragment).

OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 RN NCBI_TaxID=11320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83303830; PubMed=6612993;
 RA Parvin J.D., Young J.F., Palese P.;
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural
 RL proteins of influenza A virus isolates.";
 RL Virology 128:512-517(1993).
 DR EMBL; K00962; AAA43516.1; -.
 DR InterPro; IPR000256; Flu_NS1.
 DR Pfam; PF00600; Flu_NS1; 1.
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1811 MW; 23F434B5AEFFAD93 CRC64;
 Query Match 23.8%; Score 25; DB 12; Length 16;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 12 WKLLPENG 19
 Db |.:|:|
 2 WRSSDENG 9
 RESULT 10
 Q9F0P3 PRELIMINARY; PRT; 17 AA.
 AC Q9F0P3
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Electron transfer flavoprotein subunit A (Fragment).
 GN ETFA.
 OS Paracoccus denitrificans.
 OC Plasmid pLE20.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Paracoccus.
 OX NCBI_TaxID=266;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93388590; PubMed=8376381;
 RA Bedyk L.A., Escudero K.W., Gill R.E., Griffin K.J., Frerman F.E.;
 RT "Cloning, sequencing, and expression of the genes encoding subunits of
 RT Paracoccus denitrificans electron transfer flavoprotein.";
 RL J. Biol. Chem. 268:20211-20217(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21101849; PubMed=11160087;
 RA Pales L., Kryszak L., Zeilstra-Ryalls J.;
 RT "Control of hema Expression in Rhodobacter sphaeroides 2.4.1: Effect
 RL of a Transposon Insertion in the hbdA Gene.";
 RL J. Bacteriol. 183:1568-1576(2001).
 DR EMBL; AF212164; AAG43534.1; -.
 KW Plasmid.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1744 MW; F277E1E18F28DEA2 CRC64;
 Query Match 23.8%; Score 25; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 10 DLWKLPE 17
 Db |.:|:|
 5 DLFSVPE 12
 RESULT 11
 P82674 PRELIMINARY; PRT; 18 AA.
 ID P82674
 AC P82674
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S5 (MRP-S5) (Fragments).
 OS Bos taurus (Bovine).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Bovidae; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=LIVER;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H.,
 RA Spremulli L.L.;
 RT "Identification of four proteins from the small subunit of the
 RL mammalian mitochondrial ribosome using a proteomics approach.";
 RT Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- MASS SPECTROMETRY: MW=974.58; METHOD=ELECTROSPRAY; RANGE=1-8.
 CC -1- SIMILARITY: BELONGS TO THE SEP FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR000851; Ribosomal_S5.
 DR PROSITE; PS00585; RIBOSOMAL_S5; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_CONS 8
 FT UNSURE 17 17 OR I.
 FT NON_TER 18 18
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2127 MW; 199BC913E7E25FAF CRC64;
 Query Match 23.8%; Score 25; DB 6; Length 18;
 Best Local Similarity 57.1%; Pred. No. 3.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 7 TFSDLWK 13
 Db |.:|:|
 2 TADELWK 8
 RESULT 12
 O84129 PRELIMINARY; PRT; 18 AA.
 ID O84129
 AC O84129
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
 DE 8), COOH terminus of NS1 (Fragment).
 DE Influenzavirus A.
 OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=11320;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83303830; PubMed=6612993;
 RA Parvin J.D., Young J.F., Palese P.;
 RT "nonsense mutations affecting the lengths of the ns1 nonstructural
 RT proteins of influenza A virus isolates.";
 RL Virology 128:512-517(1993).
 DR EMBL; K00959; AAA43541.1; -.
 DR InterPro; IPR000256; Flu_NS1.
 DR Pfam; PF00600; Flu_NS1; 1.
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FEBEF CRC64;
 Query Match 23.8%; Score 25; DB 12; Length 18;
 Best Local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 12 WKLLPENG 19
 Db |.:|:|
 2 WRSSDENG 9
 RESULT 13


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022064
AC O22064 PRELIMINARY; PRT; 19 AA.
ID O22064;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoglucose isomerase (EC 5.3.1.9) (Fragment).
GN PGI.
OS Dioscorea tenuipes.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
OC Dioscorea.
OX NCBI_TaxID=64476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DTEL;
RX MEDLINE=98072503; PubMed=9409845;
RA Terauchi R., Terachi T., Miyashita N.;
RT "DNA polymorphism at the Pgi locus of a wild yam, Dioscorea tokoro.";
RL Genetics 147:1899-1914(1997).
DR EMBL; AB006004; BAA23204.1; -.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2245 MW; 333500DFC9EAD5P8 CRC64;

Query Match 23.8%; Score 25; DB 10; Length 19;
Best Local Similarity 30.8%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLQOETPSDLWLK 14
Db 1 PLGPRQLQNIWLL 13

RESULT 14
Q83965 PRELIMINARY; PRT; 19 AA.
AC Q83965;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Influenza A/Berkeley/1/68 (H2N2), non-structural protein (Seg 8), cooh
DE terminus of ns1 (Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza a virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00957; AAA43518.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; I.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2235 MW; E10F1743F4263EAE CRC64;

Query Match 23.8%; Score 25; DB 12; Length 19;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 WKLLPENG 19
Db 2 WRSSSENG 9

RESULT 15
Q9MJQ5 PRELIMINARY; PRT; 10 AA.
ID Q9MJQ5
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Q9MJQ5;
AC 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Podospora curvicolli.
OS Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=48157;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RX MEDLINE=20150243; PubMed=10684923;
RA Saguez C., Lecellier G., Koll F.;
RT "Intronic GIV-VIG endonuclease gene in the mitochondrial genome of
RT Podospora curvicolli: evidence for mobility.";
RL Nucleic Acids Res. 28:1299-1306(2000).
DR EMBL; AJ249984; CAB72447.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR PROSITE; PS00193; CYTOCHROME_B_OO; UNKNOWN_1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1200 MW; C31A223B437B0772 CRC64;

Query Match 22.9%; Score 24; DB 8; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 WKLLP 16
Db 6 WYLLP 10

Search completed: February 12, 2003, 10:44:59
Job time : 30 secs
```


GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:36:28 ; Search time 29 Seconds
(without alignments)
27.174 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLKLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1015

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	22.9	10	1	HTF_HELZE	P16353 heliothis z
2	23	21.9	10	1	AKHX_LOCFI	P81626 locusta mlg
3	22	21.0	13	1	NP2_LYMST	P80178 lymanea sta
4	22	21.0	13	1	NP2_LYMST	P80179 lymanea sta
5	22	21.0	13	1	NP4_LYMST	P80181 lymanea sta
6	22	21.0	13	1	NP5_LYMST	P80182 lymanea sta
7	22	21.0	16	1	IBP4_PIG	P24854 sus scrofa
8	21.5	20.5	12	1	UR2_SCYCA	P35490 scyllorhinu
9	21	20.0	8	1	HTF2_PERAM	P04549 periplaneta
10	21	20.0	10	1	HTF2_CARMO	P11385 carausius m
11	21	20.0	15	1	URE1_MORMO	P17337 morganella
12	21	20.0	17	1	ACT6_SOYBN	P15986 glycine max
13	21	20.0	18	1	CPAX_BOVIN	P22779 bos taurus
14	20	19.0	8	1	AKH_TABAT	P14595 tabanus atr
15	20	19.0	8	1	HTF1_PERAM	P04548 periplaneta
16	20	19.0	10	1	HTF1_TABAT	P14596 tabanus atr
17	20	19.0	13	1	NP3_LYMST	P80180 lymanea sta
18	20	19.0	17	1	PH4_PERAM	P82697 periplaneta
19	20	19.0	18	1	PCG6_PACGO	P82419 pachycondyl
20	20	19.0	19	1	AL22_HORSE	P81217 equus cabal
21	20	19.0	19	1	IRBP_CAVPO	P12666 cavia porce
22	20	19.0	19	1	PCG7_PACGO	P82420 pachycondyl
23	19	18.1	8	1	AKHG_GRYBI	P14086 gryllus bim
24	19	18.1	8	1	CLP_THICU	P80488 thioacillu
25	19	18.1	8	1	HTF_TENMO	P25419 tenebrio mo
26	19	18.1	10	1	HTF_NAUCI	P10939 nauphoeta c
27	19	18.1	10	1	URA7_HUMAN	P34990 homo sapien
28	19	18.1	15	1	CHI1_PEA	P21225 pisum sativ
29	19	18.1	15	1	LEC1_PSOSC	P22582 psophocarpu
30	19	18.1	15	1	PC20_BRANA	P81096 brassica na
31	19	18.1	16	1	ALL1_CALVO	P41839 calliphora
32	19	18.1	19	1	FIBA_ANTAM	P14440 antilocapra
33	19	18.1	19	1	HI70_RAT	P21794 rattus norv

ALIGNMENTS

RESULT 1

HTF_HELZE

ID HTF_HELZE STANDARD; PRT; 10 AA.

AC P16353;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Hypertrichalosemic hormone (HeZ-HRTH)

OS Heliothis zea (Corn earworm) (Bollworm).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;

OC Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.

OX NCBI_TaxID=7113;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=88326324; PubMed=3415690;

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,

RA Tseng C.M., Zhang Y.S., Hayes D.K.;

RT "Isolation and primary structure of a neuropeptide hormone from

RT Heliothis zea with hypertrichalosemic and adipokinetic activities.";

RL Biochem. Biophys. Res. Commun. 155:344-350(1988).

CC -!- FUNCTION: HYPERTRICHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT

CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS

CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

CC PIR; A31571; A31571.

DR InterPro: IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation.

FT MOD_RES 1 1

FT MOD_RES 10 10

SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

PYRROLIDONE CARBOXYLIC ACID.

AMIDATION.

Query Match 22.9%; Score 24; DB 1; Length 10;

Best Local Similarity 62.5%; Pred. No. 5.3e+02;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETESDLW 12

| | | |

Db 1 QLTSSGW 8

RESULT 2

AKHX_LOCFI

ID AKHX_LOCFI STANDARD; PRT; 10 AA.

AC P81626;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Peptide hormone.

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;

OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

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RN  SEQUENCE.
RC  TISSUE=corpora cardiaca;
RA  Siegart K.J.;
RL  Submitted (DEC-1998) to the SWISS-PROT data bank.
CC  -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
CC  INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.
CC  -!- SIMILARITY: SOME SIMILARITY TO THE AKH / HRTH / RPCH FAMILY.
DR  InterPro: IPR002047; AKH.
DR  PROSITE: PS00256; AKH; 1.
KW  Neuropeptide; Amidation.
FT  MOD RES 1 1
FT  MOD RES 10 10
FT  MOD RES 10 10
SQ  SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.6e+02; Length 13;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 QETFSDLW 12
Db 1 QVTFSDW 8

RESULT 3
NP1_LYMST
ID NP1_LYMST STANDARD; PRT; 13 AA.
AC P80178;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RL "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32471; S32471.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03; Length 13;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFSFD 10
Db 5 ISNSAFSD 12

RESULT 4
NP2_LYMST
ID NP2_LYMST STANDARD; PRT; 13 AA.
AC P80179;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 2.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.

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RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RL "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32472; S32472.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
FT MOD RES 13 13
FT UNSURE 8
SQ SEQUENCE 13 AA; 1492 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03; Length 13;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFSFD 10
Db 5 ISSAFSD 12

RESULT 5
NP4_LYMST
ID NP4_LYMST STANDARD; PRT; 13 AA.
AC P80181;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RL "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BB56D5B455 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03; Length 13;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFSFD 10
Db 5 ISNSAFSD 12

RESULT 6
NP5_LYMST
ID NP5_LYMST STANDARD; PRT; 13 AA.
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 5.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.

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RC ZISSUE-Ganglion;
RA MEDLINE=93238777; PubMed=8477756;
RX Johnson A.H., Rehfeld J.F.;
RT "LymnaeaDFamides, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQTFSD 10
DB 5 ISSAFSD 12

RESULT 7
IBP4_PIG
ID IBP4_PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Ethernan T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136 (1991).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR; JH0517; JH0517.
DR InterPro; IPR000867; Insl_gro_fac.pr.
DR InterPro; IPR000716; Thyroglobulin.1.
DR PROSITE; PS00222; IGF BINDING; PARTIAL.
DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;

Query Match 21.0%; Score 22; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQE 6
DB 7 PPPSEE 12

RESULT 8
UR2_SCYCA
ID UR2_SCYCA STANDARD; PRT; 12 AA.
AC P35490;

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DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RX TISSUE=Spinal cord;
RC MEDLINE=92319231; PubMed=1620290;
RA Conlon J.M., O'Harte F., Smith D.D., Balmert R.J., Hazon N.;
RT "Purification and characterization of urotensin II and parvalbumin
RT from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
RL Neuroendocrinology 55:230-235 (1992).
CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; 804729F9D579CEBA CRC64;

Query Match 20.5%; Score 21.5; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 8 PSD-LWK 13
DB 3 PSDCFWK 9

RESULT 9
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1997 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Hyperrehaloesamic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (Pea-CAH-II) (LED-CC-II) (Hyperrehaloesamic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
RN [3]

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RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches Leucophaea maderae,
 Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 and of the stick insect Extatosoma tiaratum assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A05170; A05170.
 DR PIR; S08996; S08996.
 DR PIR; B4960; B4960.
 DR PIR; B49823; B49823.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD RES 1 1
 FT MOD RES 8 8
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 Query Match 20.0%; Score 21; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 5 QETFSDLW 12
 DB 1 QLTFTPNW 8
 RESULT 10
 HTF2_CARMO
 ID HTF2_CARMO STANDARD; PRT; 10 AA.
 AC P11385;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
 neuropeptide II).
 DE Carausius morosus (Indian stick insect), and
 OS Extatosoma tiaratum (Stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Phasmatodea;
 OC Heteromellidae; Carausius.
 OX NCBI_TaxID=7022, 7024;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=87157103; PubMed=3828078;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structure of the hypertrehalosaemic factor II from the
 corpus cardiaca of the Indian stick insect, Carausius morosus,
 determined by fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches Leucophaea maderae,

RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 and of the stick insect Extatosoma tiaratum assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=93129188; PubMed=1482345;
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
 RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
 a stick insect corpus cardiaca.";
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; S07157; S07157.
 DR PIR; S09138; S09138.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Glycoprotein.
 FT MOD RES 1 1
 FT MOD RES 8 8
 FT MOD RES 10 10
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;
 Query Match 20.0%; Score 21; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 5 QETFSDLW 12
 DB 1 QLTFTPNW 8
 RESULT 11
 UREL_MORMO
 ID UREL_MORMO STANDARD; PRT; 15 AA.
 AC P17337;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Urease 63 kDa
 subunit) (Fragment).
 DE URE.
 GN Morganella morganii (Proteus morganii).
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 isolation of gene sequences.";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- COFACTOR: Binds 2 nickel ions per subunit (potential).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
 DR PIR; A35389; A35389.
 DR InterPro; IPR001924; UreaseA.
 DR PROSITE; PS00145; UREASE 2; PARTIAL.
 DR PROSITE; PS01120; UREASE 1; PARTIAL.
 KW Hydrolase; Metal-binding; Nickel.
 FT NON_TER 15 15
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1650 MW; 09E27AA54241687B CRC64;
 Query Match 20.0%; Score 21; DB 1; Length 15;
 Best Local Similarity 25.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQETPSDLW 12
 Db 1 FOISQEQYGGULF 12

RESULT 12
 ACT6 SOYBN
 ID ACT6 SOYBN STANDARD; PRT; 17 AA.
 AC P15986;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin 6 (Fragment).
 GN SAG6.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RX MEDLINE=91346640; PubMed=2102831;
 RA Pearson L., Meagher R.B.;
 RT "Diverse soybean actin transcripts contain a large intron in the 5'
 untranscribed leader: structural similarity to vertebrate muscle actin
 genes.";
 RL Plant Mol. Biol. 14:513-526(1990).
 CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
 IN ALL EUKARYOTIC CELLS.
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
 IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
 CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.

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 EMBL; X17119; CAA34979.1; -
 DR PIR; S15754; S15754.
 DR InterPro; IPR004001; Actin.
 DR InterPro; IPR004000; Actin_like.
 DR Pfam; PF00022; actin; 1.
 DR PROSITE; PS00406; ACTINS 1; PARTIAL.
 DR PROSITE; PS00432; ACTINS 2; PARTIAL.
 DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT NON_TER 17
 FT SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match 20.0%; Score 21; DB 1; Length 17;
 Best Local Similarity 40.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 DLWKLKLPENG 19
 Db 6 DIQPLVCDNG 15

RESULT 13
 CPAX BOVIN
 ID CPAX BOVIN STANDARD; PRT; 18 AA.
 AC P22779;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91027757; PubMed=2121272;
 RA Lazard D., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
 RT "Identification and biochemical analysis of novel olfactory-specific
 cytochrome P-450IIA and UDP-glucuronosyl transferase.";
 RL Biochemistry 29:7433-7440(1990).
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 MONOOXYGENASES. IN LIVER MICROSOMES THIS ENZYME IS INVOLVED IN AN
 NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 ACIDS, AND XENOBIOTICS.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR; A35704; A35704.
 DR InterPro; IPR001128; Cytochrome P450.
 DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum; Olfaction.
 FT NON_TER 1
 FT VARIANT 6 6 G -> D.
 FT VARIANT 11 11 A -> E.
 FT NON_TER 18 18
 FT SEQUENCE 18 AA; 2058 MW; F80746F76CCD77FF CRC64;

Query Match 20.0%; Score 21; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 2.9e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 PPLSQETPSDL 11
 Db 5 FQFQQQAKEL 15

RESULT 14
 AKH TABAT
 ID AKH TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
 DE (DCC I).
 DE Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Tabanomorpha; Tabanidae; Tabanus.
 OC NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 hypotrehalosemic activity isolated from the corpora cardiaca of horse
 flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A33995; A33995.

DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 Query Match 19.0%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 5 QETFSDLW 12
 Db 1 QUTFTPGW 8

RESULT 15
 HTF1_PERAM
 ID HTF1_PERAM STANDARD; PRT; 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
 DE (PeA-CAH-I) (LeD-CC-I) (Hypertrehalosaemic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry";
 RL Biochem. Biophys. Res. Commun. 124:350-358 (1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579 (1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical";
 RL Peptides 10:1287-1289 (1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
 CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).

CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A05169; A05169.
 DR PIR; S08995; S08995.
 DR PIR; A49823; A49823.
 DR PIR; A44960; A44960.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 19.0%; Score 20; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 QETFSDLW 12
 Db 1 QVNFSPNW 8

Search completed: February 12, 2003, 10:44:24
 Job time : 30 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	34	32.4	19	2	B61409	genome polyprotein
2	26	24.8	18	2	A9396	Tha p 1 - Thaumeto
3	25	23.8	14	2	A35105	hypothetical prote
4	25	23.8	15	2	PA0110	translation elonga
5	24	22.9	10	2	A31571	hypertrehalosemic/
6	24	22.9	11	2	S41747	chaperonin 10 homo
7	23	21.9	8	2	S11545	adipokinetic hormo
8	23	21.9	9	2	A24244	adipokinetic hormo
9	23	21.9	15	2	S20410	protein kinase (EC
10	22	21.0	5	2	S70615	endo-1,4-beta-xyla
11	22	21.0	8	2	S16324	hypothetical prote
12	22	21.0	13	2	S32471	lynnadPamide 1 - 9
13	22	21.0	13	2	S32472	lynnadPamide 2 - 9
14	22	21.0	13	2	S32474	lynnadPamide 4 - 9
15	22	21.0	13	2	S32475	lynnadPamide 5 - 9
16	22	21.0	14	2	B48954	L-2,4-diaminobutyr
17	22	21.0	16	2	JH0517	insulin-like growt
18	22	21.0	17	2	SS9481	hydroxyproline-ric
19	21.5	20.5	14	2	PH1625	Ig H chain V-D-J r
20	21.5	20.5	15	2	PH1788	T cell receptor al
21	21.5	20.5	18	2	I40062	shikimate 5-dehydr
22	21	20.0	8	2	S08996	hypertrehalosemic
23	21	20.0	8	2	B49823	adipokinetic hormo
24	21	20.0	10	2	JC1416	neuropeptide Ied-C
25	21	20.0	10	2	S09138	hypertrehalosemic
26	21	20.0	10	2	S53789	hypertrehalosemic
27	21	20.0	11	2	P33098	neuropeptide Pec-H
28	21	20.0	10	2	P33098	214K exoantigen (v
29	21	20.0	11	2	S53436	beta-D-galactosida

RESULT 3

Wed Feb 12 11:22:41 2003

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A35105
hypothetical protein - Neurospora crassa mitochondrion (fragment)
C:Species: mitochondrion Neurospora crassa
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C:Accession: A35105
R:Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A:Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora m
A:Reference number: A35105; MUID:90263093; PMID:2160856
A:Accession: A35105
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-14 <SAV>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 23.8%; Score 25; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 1.3e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 5;

QY 9 SDLWLLPENG 19
DB 2 SFELLLQLKG 12

RESULT 4
PA0110
translation elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 26-Apr-1996
C:Accession: PA0110
R:Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0110
A:Molecule type: protein
A:Residues: 1-15 <RAM>

Query Match 23.8%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 7 TFSDL 11
DB 3 TFSDL 7

RESULT 5
A31571
hypertrehalosemic/adipokinetic hormone - bollworm
N:Alternate names: Hez-HrTH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C:Accession: A31571
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
Biochem. Biophys. Res. Commun. 155, 344-350, 1988
A:Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea w
A:Reference number: A31571; MUID:88326324; PMID:3415690
A:Accession: A31571
A:Molecule type: protein
A:Residues: 1-10 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 22.9%; Score 24; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.3e+03; Indels 3; Gaps 0;
Matches 5; Conservative 0; Mismatches 3;

QY 5 SDLW 12

us-09-403-440a-2.closed.rpr

Db 1 QLTFSGW 8

RESULT 6
S41747
chaperonin 10 homolog - potato (fragment)
C:Species: Solanum tuberosum (potato)
C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999
C:Accession: S41747
R:Burt, W.J.E.; Leaver, C.J.
FEBS Lett. 339, 139-141, 1994
A:Title: Identification of a chaperonin-10 homologue in plant mitochondria.
A:Reference number: S41747; MUID:94148071; PMID:7906228
A:Accession: S41747
A:Molecule type: protein
A:Residues: 1-11 <BUR>
A:Experimental source: mitochondrion
C:Keywords: mitochondrion; molecular chaperone

Query Match 22.9%; Score 24; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1;

QY 14 LLPENG 19
DB 2 LLPYG 7

RESULT 7
S11545
adipokinetic hormone - nestling-sucking blowfly
C:Species: Protophormia terraenovae (nestling-sucking blowfly)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997
C:Accession: S11545
R:Gaede, G.; Wilps, H.; Kellner, R.
Biochem. J. 269, 309-313, 1990
A:Title: Isolation and structure of a novel charged member of the red-pigment-concentra
erraenovae (Diptera).
A:Reference number: S11545; MUID:90351345; PMID:2386478
A:Accession: S11545
A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 2.8e+05; Indels 3; Gaps 0;
Matches 5; Conservative 0; Mismatches 3;

QY 5 OETFSDLW 12
DB 1 QLTFSPDW 8

RESULT 8
A24244
adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
C:Accession: A24244
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgwa
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heli
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutami

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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 QETPSDLW 12
Db 1 QLTFTSSW 8

RESULT 9

S20410
Lymnaea stagnalis - spinach chloroplast (fragment)
N;Alternate names: LHCII protein kinase
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S20410
R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992
A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cytochrome b6/f complex; light-harvesting complex; membrane-associated complex; photosystem II; photosynthesis
A;Reference number: S20410; MUID:92183823; PMID:1544419
A;Accession: S20410
A;Molecule type: protein
A;Residues: 1-15 <GAL>
C;Genetics:
A;Genome: chloroplast
C;Function:
A;Description: is responsible for the regulation of energy distribution between photosystems II and I
A;Note: does not exhibit redox-controlled activation
C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; photosynthesis

Query Match 21.9%; Score 23; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PPLSQETPSD 10
Db 5 PDVEXSTUSD 14

RESULT 10

S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)
N;Alternate names: xylanase
C;Species: Streptomyces sp.
A;Variety: Chainia sp. NCL 82.5.1
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70615
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A;Title: Structural environment of an essential cysteine residue of xylanase from Chainia sp.
A;Reference number: S70615; MUID:96265041; PMID:8670151
A;Accession: S70615
A;Molecule type: protein
A;Residues: 1-5 <RAO>
A;Experimental source: Chainia sp. strain NCL 82.5.1
A;Note: the source is designated as Chainia sp.
C;Function:
A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A;Pathway: fermentation of hemicellulose into ethanol
C;Keywords: glycosidase; hydrolase

Query Match 21.0%; Score 22; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ETFSFD 10
Db 1 ETFXD 5

RESULT 11

S16324
hypothenical protein 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
C;Accession: S16324
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991
A;Title: A novel class of plant proteins containing a homeodomain with a closely linked homeobox domain
A;Reference number: S16323; MUID:91266907; PMID:1675603
A;Accession: S16324
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <RUB>
A;Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 21.0%; Score 22; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 WKLLP 16
Db 3 YKLLP 7

RESULT 12

S32471
Lymnaea stagnalis - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S32471
R;Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A;Title: Lymnaea stagnalis, a new family of neuropeptides from the pond snail, Lymnaea stagnalis
A;Reference number: S32471; MUID:93238777; PMID:8477756
A;Accession: S32471
A;Molecule type: protein
A;Residues: 1-13 <JOH>
A;Cross-references: PIDN:AAB26362.1; PID:g299829
A;Experimental source: ganglia
C;Keywords: amidated carboxyl end; neuropeptide
F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSQETPSD 10
Db 5 ISNSAFSD 12

RESULT 13

S32472
Lymnaea stagnalis - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S32472
R;Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A;Title: Lymnaea stagnalis, a new family of neuropeptides from the pond snail, Lymnaea stagnalis
A;Reference number: S32471; MUID:93238777; PMID:8477756
A;Accession: S32472
A;Molecule type: protein
A;Residues: 1-13 <JOH>
A;Cross-references: PIDN:AAB26363.1; PID:g299830
A;Experimental source: ganglia
C;Keywords: amidated carboxyl end; neuropeptide
F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

us-09-403-440a-2.closed.rpr

Wed Feb 12 11:22:41 2003

Qy 3 LSQETFS 10
:|
Db 5 ISSSAFSD 12

RESULT 14

S32474
Lymnaeidae 4 - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C:Accession: S32474
R:Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A:Title: Lymnaeidae, a new family of neuroleptids from the pond snail, Lymnaea stagnalis
A:Reference number: S32471; MUID:93238777; PMID:8477756
A:Accession: S32474
A:Molecule type: protein
A:Residues: 1-13 <JOH>
A:Cross-references: PIDN:AAB26365.1; PID:g299832
A:Experimental source: ganglia
C:Keywords: amidated carboxyl end; neuroleptide
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFS 10
:|
Db 5 ISSSAFSD 12

RESULT 15

S32475
Lymnaeidae 5 - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C:Accession: S32475
R:Johnsen, A.H.; Rehfeld, J.F.
Eur. J. Biochem. 213, 875-879, 1993
A:Title: Lymnaeidae, a new family of neuroleptids from the pond snail, Lymnaea stagnalis
A:Reference number: S32471; MUID:93238777; PMID:8477756
A:Accession: S32475
A:Molecule type: protein
A:Residues: 1-13 <JOH>
A:Cross-references: PIDN:AAB26366.1; PID:g299833
A:Experimental source: ganglia
C:Keywords: amidated carboxyl end; neuroleptide
F:13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.0%; Score 22; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LSQETFS 10
:|
Db 5 ISSSAFSD 12

Search completed: February 12, 2003, 10:45:51
Job time : 47 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:34:07 ; Search time 14 Seconds
(without alignments)
39.931 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQTFSDLWKLLPENG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	20	4	US-09-081-975-8
2	99	94.3	20	4	US-09-081-975-10
3	99	94.3	20	4	US-09-081-975-11
4	99	94.3	20	4	US-09-081-975-16
5	99	94.3	64	1	US-08-245-500A-1
6	99	94.3	64	1	US-08-390-546-1
7	99	94.3	64	1	US-08-390-479A-1
8	99	94.3	64	1	US-08-557-393-1
9	99	94.3	64	1	US-08-390-516C-1
10	99	94.3	64	1	US-08-390-517A-1
11	99	94.3	64	1	US-08-390-515A-1
12	99	94.3	64	2	US-08-801-718-1
13	99	94.3	64	4	US-09-170-159A-1
14	99	94.3	261	4	US-09-414-436-3
15	99	94.3	363	2	US-08-697-221-17
16	99	94.3	363	2	US-08-697-221-18
17	99	94.3	363	2	US-08-697-221-19
18	99	94.3	363	2	US-08-697-221-20
19	99	94.3	363	2	US-08-697-221-21
20	99	94.3	363	2	US-08-697-221-22
21	99	94.3	363	2	US-08-697-221-23
22	99	94.3	363	2	US-08-697-221-24
23	99	94.3	393	1	US-08-047-041A-25
24	99	94.3	393	1	US-08-047-041A-26
25	99	94.3	393	1	US-08-047-041A-27
26	99	94.3	393	1	US-08-047-041A-28
27	99	94.3	393	1	US-08-347-792-2

28 99 94.3 393 1 US-08-390-516C-6 Sequence 6, Appli
29 99 94.3 393 1 US-08-390-516C-7 Sequence 7, Appli
30 99 94.3 393 1 US-08-390-516C-8 Sequence 8, Appli
31 99 94.3 393 1 US-08-390-516C-9 Sequence 9, Appli
32 99 94.3 393 1 US-08-431-357-2 Sequence 2, Appli
33 99 94.3 393 1 US-08-390-515A-6 Sequence 6, Appli
34 99 94.3 393 1 US-08-390-515A-7 Sequence 7, Appli
35 99 94.3 393 1 US-08-390-515A-8 Sequence 8, Appli
36 99 94.3 393 1 US-08-390-515A-9 Sequence 9, Appli
37 99 94.3 393 2 US-08-795-006A-32 Sequence 32, Appli
38 99 94.3 393 2 US-08-697-221-2 CITY: Boston
39 99 94.3 393 2 US-08-697-221-3 CITY: Boston
40 99 94.3 393 2 US-08-697-221-4 STATE: MA
41 99 94.3 393 2 US-08-697-221-11 COUNTRY: USA
42 99 94.3 393 2 US-08-697-221-12 ZIP: 02110
43 99 94.3 393 2 US-08-697-221-13 COMPUTER READABLE FORM:
44 99 94.3 393 2 US-08-697-221-14 MEDIUM TYPE: Diskette
45 99 94.3 393 2 US-08-697-221-15 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-081-975-8

ALIGNMENTS

RESULT 1
US-09-081-975-8
; Sequence 8, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-081-975-8

Query Match 94.3%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLEN 19

RESULT 2

US-09-081-975-10
 ; Sequence 10, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP
 ; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081,975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eisenstein, Ronald I
 ; REGISTRATION NUMBER: 30,628
 ; REFERENCE/DOCKET NUMBER: 47400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-6054
 ; TELEFAX: 617-345-1300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-081-975-10

Query Match 94.3%; Score 99; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLEN 19

RESULT 3

US-09-081-975-11
 ; Sequence 11, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP

; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081,975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eisenstein, Ronald I
 ; REGISTRATION NUMBER: 30,628
 ; REFERENCE/DOCKET NUMBER: 47400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-345-6054
 ; TELEFAX: 617-345-1300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-081-975-11

Query Match 94.3%; Score 99; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 2 PPLSQETFSDLWKLLEN 19

RESULT 4

US-09-081-975-16
 ; Sequence 16, Application US/09081975
 ; Patent No. 6451979
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING
 ; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon Peabody LLP
 ; STREET: 101 Federal Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/081,975
 ; FILING DATE: 12-MAY-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/046,207
 ; FILING DATE: 12-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:


```

RESULT 7
US-08-390-479A-1
; Sequence 1, Application US/08390479A
; Patent No. 5618921
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,479A
; FILING DATE: 02-FEB-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48992
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
;
US-08-390-479A-1
Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PLSQETFSDLWKLLPEN 18
Db 12 PLSQETFSDLWKLLPEN 29

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RESULT 8
US-08-557-393-1
; Sequence 1, Application US/08557393
; Patent No. 5702903
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,393
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,500
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
;
US-08-557-393-1
Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PLSQETFSDLWKLLPEN 18
Db 12 PLSQETFSDLWKLLPEN 29

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RESULT 9
US-08-390-516C-1
; Sequence 1, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
; US-08-390-516C-1

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```

Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

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RESULT 10
US-08-390-517A-1
; Sequence 1, Application US/08390517A
; Patent No. 5736338
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,517A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
; US-08-390-517A-1

```

```

Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

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RESULT 11
US-08-390-515A-1
; Sequence 1, Application US/08390515A
; Patent No. 5756455
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,515A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 64 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

;
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17q
US-08-390-515A-1

Query Match 94.3%; Score 99; DB 1; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 PPLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 12
US-08-801-718-1
; Sequence 1, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17q

US-08-801-718-1
Query Match 94.3%; Score 99; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;

Matches 18; Conservative 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 12
US-08-801-718-1
; Sequence 1, Application US/08801718
; Patent No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17q

US-08-801-718-1
Query Match 94.3%; Score 99; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 PPLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 13
US-09-170-159A-1
; Sequence 1, Application US/09170159A
; Patent No. 6399755
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,159A
FILING DATE: 13-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17q
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-170-159A-1

Query Match 94.3%; Score 99; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
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Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 14
US-09-414-436-3
; Sequence 3, Application US/09414436
; Patent No. 6294384

;; GENERAL INFORMATION:
;; APPLICANT: Dell'Acqua, Giorgio
;; APPLICANT: Mann, Michael J.
;; APPLICANT: Dzaou, Victor J.
;; TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
;; FILE REFERENCE: p53f
;; CURRENT APPLICATION NUMBER: US/09/414,436
;; CURRENT FILING DATE: 1999-10-07
;; EARLIER APPLICATION NUMBER: 60/103,849
;; EARLIER FILING DATE: 1999-10-09
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 3
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-414-436-3

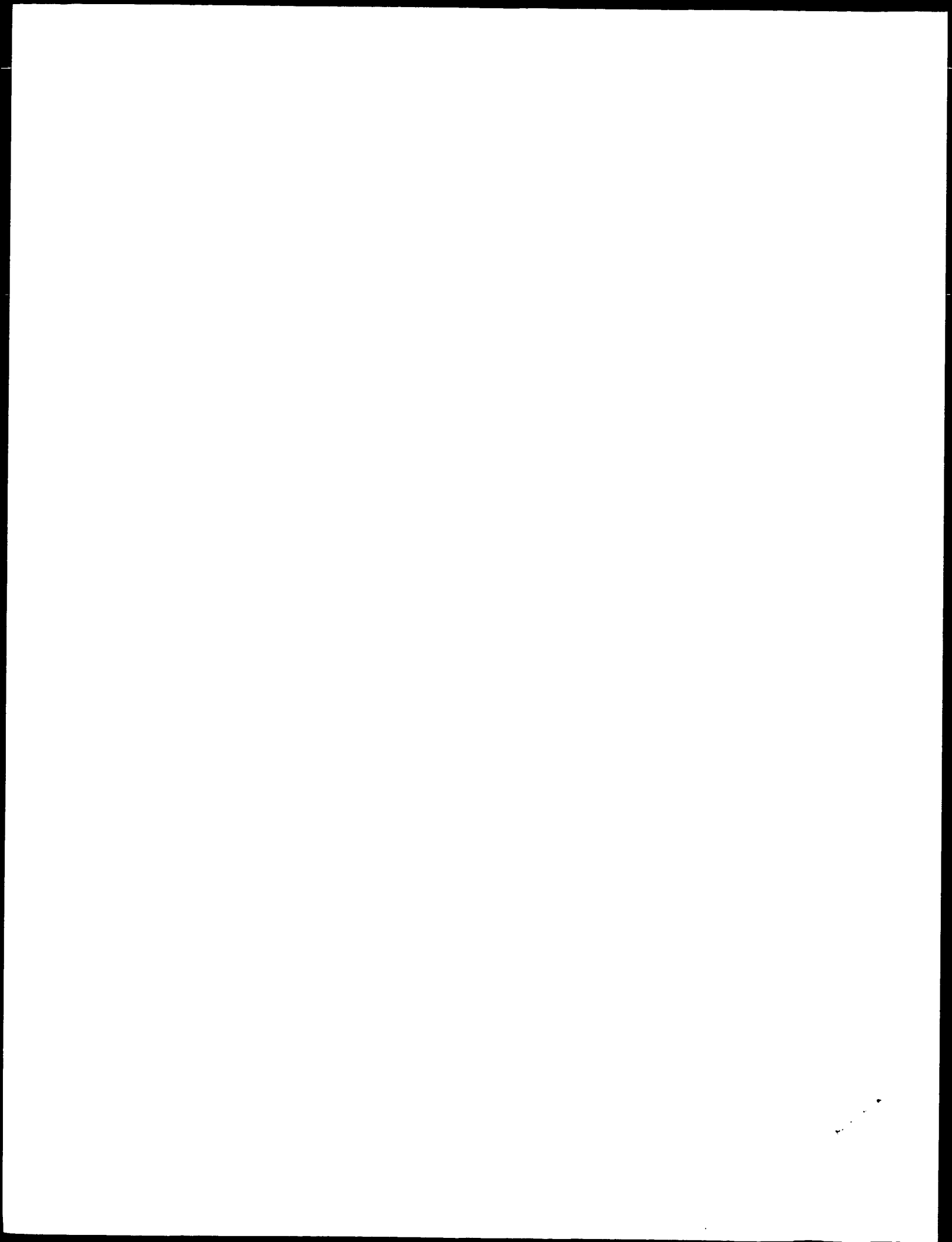
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 15
US-08-697-221-17
;; Sequence 17, Application US/08697221
;; Patent No. 5847083
;; GENERAL INFORMATION:
;; APPLICANT: Halazonetis, Thanos D.
;; TITLE OF INVENTION: Modified p53 Constructs and Uses
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Howson and Howson
;; STREET: Spring House Corporate Cntr., PO Box 457
;; CITY: Spring House
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19477
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/697,221
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/004,802
;; FILING DATE: 22-SEP-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kodroff, Cathy A.
;; REGISTRATION NUMBER: 33,980
;; REFERENCE/DOCKET NUMBER: WST64AUSA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-540-9206
;; TELEFAX: 215-540-5818
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 363 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-697-221-17

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Best Local Similarity 100.0%; Pred. No. 4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 12 PPLSQETFSDLWKLLPEN 29
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Job time : 15 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:35:07 ; Search time 19 Seconds
(without alignments)
83.787 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

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Total number of hits satisfying chosen parameters: 425801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	99	94.3	351	5	US-09-724-676-56463
3	99	94.3	353	5	US-09-849-602-24
4	99	94.3	393	1	PCT-US02-21461-3
5	99	94.3	393	5	US-09-860-286-9
6	99	94.3	393	6	US-10-274-874-4
7	99	94.3	393	7	US-60-423-552-118
8	99	94.3	393	7	US-60-427-579-118
9	92	87.6	19	7	US-60-438-805-9
10	91	86.7	32	6	US-10-276-774-2505
11	81	77.1	15	6	US-10-211-088-141
12	70	66.7	13	5	US-09-701-080C-22
13	70	66.7	13	5	US-09-701-080C-27
14	59	56.2	11	5	US-09-189-702A-286
15	51.5	49.0	927	6	US-10-218-140-250
16	51.5	49.0	1009	6	US-10-257-022-5
17	50	47.6	1879	6	US-10-072-012-220
18	46	43.8	422	6	US-10-209-582-898
19	46	43.8	422	6	US-10-233-553-25
20	46	43.8	422	6	US-10-233-553-26
21	46	43.8	422	6	US-10-233-553-27
22	46	43.8	422	6	US-10-233-553-28
23	44	41.9	116	1	PCT-US02-32727-30728
24	44	41.9	260	1	PCT-US02-32727-2767
25	44	41.9	260	6	US-10-057-498-2767
26	44	41.9	397	1	PCT-US02-40225-3137

27 44 41.9 397 6 US-10-320-797-3137 Sequence 3137, Ap
28 44 41.9 434 6 US-10-092-411A-4695 Sequence 4695, Ap
29 44 41.9 837 1 PCT-US02-32851-7 Sequence 7, Appli
30 44 41.9 2828 6 US-10-072-012-607 Sequence 607, App
31 44 41.9 2828 6 US-10-072-012-608 Sequence 608, App
32 44 41.9 2828 6 US-10-301-822-49 Sequence 49, Appl
33 43.5 41.4 70 1 PCT-US02-32727-3470 Sequence 3470, Ap
34 43.5 41.4 70 6 US-10-057-498-3470 Sequence 3470, Ap
35 43 41.0 264 6 US-10-245-539-6 Sequence 6, Appli
36 43 41.0 1481 5 US-09-724-676-77164 Sequence 77164, A
37 43 41.0 1481 5 US-09-724-676-77166 Sequence 77166, A
38 43 41.0 1481 5 US-09-724-676A-77164 Sequence 77166, A
39 43 41.0 1724 6 US-10-163-587A-17 Sequence 17, Appl
40 43 41.0 1763 6 US-10-276-781-1032 Sequence 1032, Ap
41 43 41.0 1763 6 US-10-276-781-1032 Sequence 1032, Ap
42 42.5 40.5 612 1 PCT-US02-32851-29 Sequence 29, Appl
43 42.5 40.5 617 1 PCT-US03-01363-156 Sequence 156, App
44 42 40.0 208 6 US-10-264-237-2160 Sequence 2160, Ap
45 42 40.0 271 5 US-09-724-676-80344 Sequence 80344, A

ALIGNMENTS

RESULT 1
US-09-724-676-56463
; Sequence 56463, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56463
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-56463

Query Match 94.3%; Score 99; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 2
US-09-724-676A-56463
; Sequence 56463, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56463
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-56463

Query Match 94.3%; Score 99; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
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US-10-274-874-4
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-874-4

Query Match 94.3%; Score 99; DB 6; Length 393;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
| | | | | | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 7

US-60-423-552-118
; Sequence 118, Application US/60423552
; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES
; FILE REFERENCE: AM101250L
; CURRENT APPLICATION NUMBER: US/60/423,552
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-423-552-118

Query Match 94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
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Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 8

US-60-427-579-118
; Sequence 118, Application US/60427579
; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES
; FILE REFERENCE: AM101250L
; CURRENT APPLICATION NUMBER: US/60/427,579
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-427-579-118

Query Match 94.3%; Score 99; DB 7; Length 393;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
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Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 9

US-60-438-805-9
; Sequence 9, Application US/60438805
; GENERAL INFORMATION:
; APPLICANT: KODASEK, THOMAS
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS
; FILE REFERENCE: UTSD:935USE1
; CURRENT APPLICATION NUMBER: US/60/438,805
; CURRENT FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-60-438-805-9

Query Match 87.6%; Score 92; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLPEN 18
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Db 1 PLSQETFSDLWKLLPEN 17

RESULT 10

US-10-276-774-2505
; Sequence 2505, Application US/10276774
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2505
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2505

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Best Local Similarity 94.4%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
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Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 11

US-10-211-088-141
; Sequence 141, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589

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; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-141

Query Match          77.1%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLL 15
Db 1 PPLSQETFSDLWKLL 15

RESULT 12
US-09-701-080C-22
; Sequence 22, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from p53
US-09-701-080C-22

Query Match          66.7%; Score 70; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SQETFSDLWKLLP 16
Db 1 SQETFSDLWKLLP 13

RESULT 13
US-09-701-080C-27
; Sequence 27, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300
; FILE REFERENCE: N73477C GCW
; CURRENT APPLICATION NUMBER: US/09/701,080C
; CURRENT FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; PRIOR FILING DATE: 1999-01-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from p53
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Best Local Similarity 100.0%; Pred. No. 9.6e-05;
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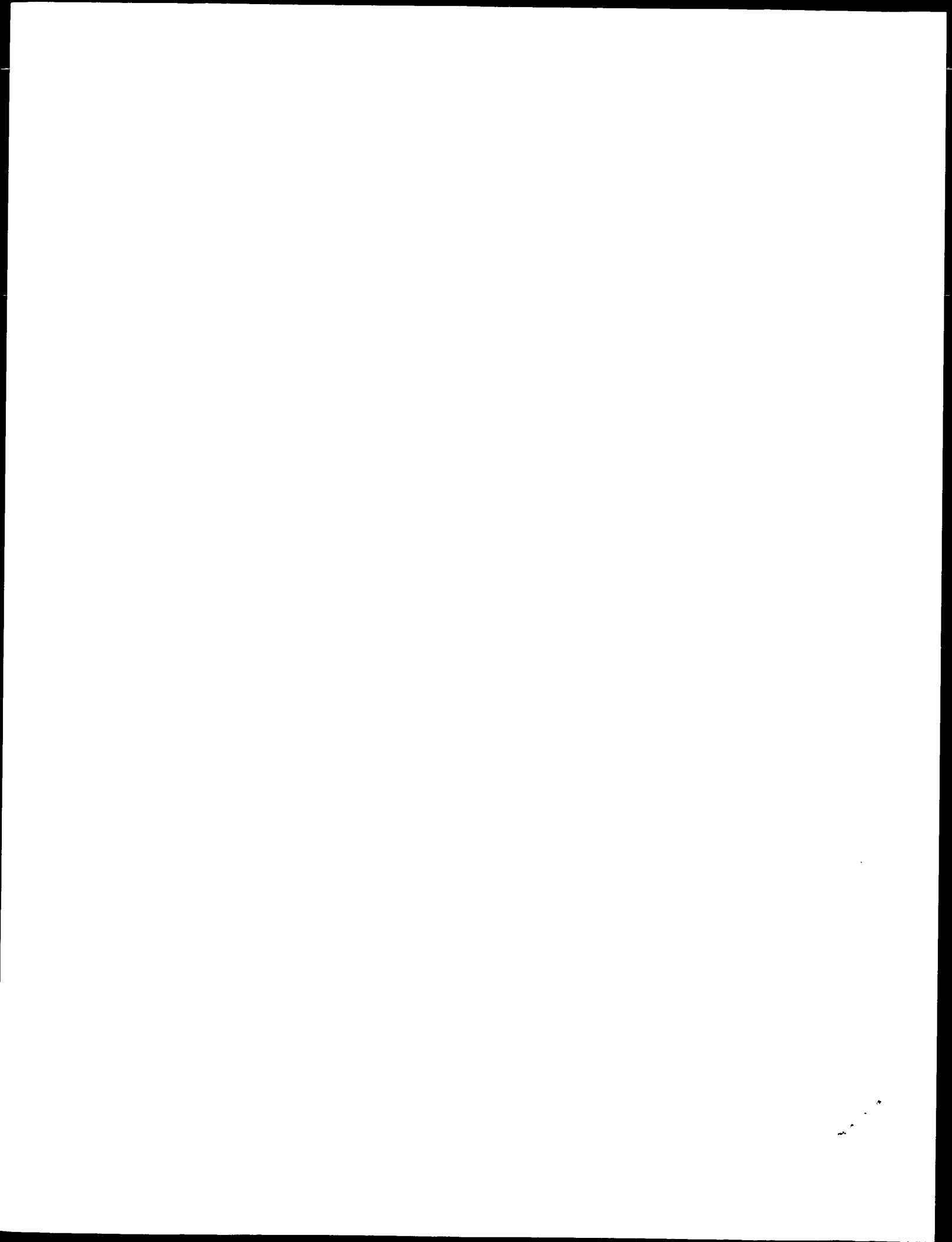
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RESULT 14
US-09-189-702A-286
; Sequence 286, Application US/09189702A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Kast, W. Martin
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune, Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 39963-20019.20
; CURRENT APPLICATION NUMBER: US/09/189,702A
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 286
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53.14 peptide 34.0324
US-09-189-702A-286

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Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LSQETFSDLWK 13
Db 1 LSQETFSDLWK 11

RESULT 15
US-10-218-140-250
; Sequence 250, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: CuraNator Version 1.0
; SEQ ID NO 250
; LENGTH: 927
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-140-250
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 10:35:42 ; Search time 11 Seconds
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44.130 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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5	99	94.3	20	US-10-155-059-16
6	99	94.3	393	US-09-776-695-32
7	99	94.3	393	US-09-732-384-3
8	99	94.3	393	US-09-860-211-9
9	99	94.3	394	US-10-155-059-4
10	94	89.5	20	US-10-155-059-14
11	94	89.5	20	US-10-155-059-15
12	93	88.6	22	US-09-214-371-73
13	92	87.6	19	US-09-732-384-7
14	90	85.7	19	US-10-155-059-13
15	89	84.8	19	US-09-214-371-1
16	86	81.9	20	US-10-155-059-19
17	77	73.3	15	US-09-732-384-6
18	74	70.5	16	US-10-155-059-23
19	74	70.5	20	US-10-155-059-20

20	72	68.6	20	12	US-10-155-059-18	Sequence 18, Appl
21	66	62.9	12	10	US-09-214-371-17	Sequence 17, Appl
22	65	61.9	15	10	US-09-950-692-6	Sequence 6, Appli
23	60	57.1	18	12	US-10-155-059-22	Sequence 22, Appl
24	59	56.2	16	10	US-09-214-371-39	Sequence 39, Appli
25	57	54.3	14	9	US-10-024-123-7	Sequence 7, Appli
26	55	52.4	12	10	US-09-214-371-7	Sequence 7, Appli
27	54	51.4	12	10	US-09-214-371-24	Sequence 24, Appl
28	54	51.4	16	10	US-09-214-371-41	Sequence 41, Appl
29	53	50.5	16	10	US-09-214-371-40	Sequence 40, Appl
30	49	46.7	12	10	US-09-214-371-25	Sequence 25, Appl
31	49	46.7	12	10	US-09-214-371-26	Sequence 26, Appl
32	48	45.7	14	10	US-09-214-371-33	Sequence 33, Appl
33	48	45.7	14	10	US-09-214-371-34	Sequence 34, Appl
34	47	44.8	10	12	US-10-155-059-17	Sequence 17, Appl
35	47	44.8	16	10	US-09-019-679-3	Sequence 3, Appli
36	46	43.8	186	10	US-09-811-284-130	Sequence 130, App
37	46	43.8	396	9	US-10-078-770-172	Sequence 172, App
38	45	42.9	837	9	US-10-045-792-12	Sequence 12, Appl
39	44	41.9	11	12	US-10-155-059-21	Sequence 21, Appl
40	44	41.9	12	10	US-09-214-371-20	Sequence 20, Appl
41	44	41.9	2828	10	US-09-905-129-21	Sequence 21, Appl
42	44	41.9	2828	10	US-09-991-630-21	Sequence 21, Appl
43	42.5	40.5	135	9	US-09-796-692-2384	Sequence 2384, Ap
44	42	40.0	15	12	US-10-155-059-24	Sequence 24, Appli
45	42	40.0	573	9	US-09-954-433-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-214-371-74
; Sequence 74, Application US/09214371B
; Patent No. US2001001851A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-74

Query Match 94.3%; Score 99; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 2

US-10-155-059-8
; Sequence 8, Application US/10155059
; Patent No. US20020147173A1

GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8
Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19
RESULT 3
US-10-155-059-10
Sequence 10, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-155-059-8
Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19
RESULT 4
US-10-155-059-11
Sequence 11, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10
Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10
Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19
RESULT 4
US-10-155-059-11
Sequence 11, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-155-059-10
Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-155-059-11

Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred.No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5
US-10-155-059-16
; Sequence 16, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine

TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THERE TO, AND USES OF THE
ANTIBODIES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628

REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-155-059-16

Query Match 94.3%; Score 99; DB 12; Length 20;
Best Local Similarity 100.0%; Pred.No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PPLSQETFSDLWKLLPEN 18
Db 2 PPLSQETFSDLWKLLPEN 19
RESULT 6
US-09-776-695-32
; Sequence 32, Application US/09776695
; Patent No. US20020068283A1
; GENERAL INFORMATION:
; APPLICANT: Boeke, Jef
; Brachmann, Rainer

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,695
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE: 2001-03-28
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141

REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-776-695-32

Query Match 94.3%; Score 99; DB 10; Length 393;
Best Local Similarity 100.0%; Pred.No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29
RESULT 7
US-09-732-384-3

; Sequence 3, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; Gu, Jidie

TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044

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; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-384-3

Query Match      94.3%; Score 99; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 12 PPLSQETFSDLWKLLPEN 29
   |||||

RESULT 8
US-09-860-211-9
; Sequence 9, Application US/09860211
; Patent No. US20020137212A1
; GENERAL INFORMATION:
; APPLICANT: Gregory, Richard J.
; Maneval, Daniel C.
; TITLE OF INVENTION: Recombinant Adenoviral Vector and
; Methods of Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/860,211
; FILING DATE: 18-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/328,673
; FILING DATE: 15-FEB-2000
; APPLICATION NUMBER: US 08/142,669
; FILING DATE: 25-OCT-1993
; APPLICATION NUMBER: US 08/233,669
; FILING DATE: 26-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy S.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 016930-000920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..393
; OTHER INFORMATION: /note= "human p53"
;

; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-384-3

Query Match      94.3%; Score 99; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 12 PPLSQETFSDLWKLLPEN 29
   |||||

RESULT 9
US-10-155-059-4
; Sequence 4, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-155-059-4

Query Match      94.3%; Score 99; DB 12; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
Db 12 PPLSQETFSDLWKLLPEN 29
   |||||

RESULT 10
US-10-155-059-14
; Sequence 14, Application US/10155059
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Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-155-059-14
Query Match 89.5%; Score 94; DB 12; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PPLSQETFSDLWKLLEN 18
Db 2 PPLSQETFSDLWKLLEN 19
RESULT 11
US-10-155-059-15
Sequence 15, Application US/10155059
Patent No. US20020147173A1
GENERAL INFORMATION:
APPLICANT: Kaelin, William
Jost, Christine
TITLE OF INVENTION: METHODS OF TREATMENT USING
NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
ANTIBODIES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Peabody LLP
STREET: 101 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-155-059-14
Query Match 89.5%; Score 94; DB 12; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PPLSQETFSDLWKLLEN 18
Db 2 PPLSQETFSDLWKLLEN 19
RESULT 12
US-09-214-371-73
Sequence 73, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pinksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 73
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Biotin-Ser
US-09-214-371-73
Query Match 88.6%; Score 93; DB 10; Length 22;

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/155,059
FILING DATE: 24-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/081,975
FILING DATE: 12-MAY-1998
APPLICATION NUMBER: 60/046,207
FILING DATE: 12-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
REGISTRATION NUMBER: 30,628
REFERENCE/DOCKET NUMBER: 47400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-6054
TELEFAX: 617-345-1300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-155-059-15
Query Match 89.5%; Score 94; DB 12; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PPLSQETFSDLWKLLEN 18
Db 2 PPLSQETFSDLWKLLEN 19
RESULT 12
US-09-214-371-73
Sequence 73, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pinksley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 73
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Biotin-Ser
US-09-214-371-73
Query Match 88.6%; Score 93; DB 10; Length 22;

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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:32:16 ; Search time 36 Seconds
(without alignments)
70.327 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLPPENG 19

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	19	AAW82321	p53 homologue TIP
2	105	100.0	19	AAW82319	p53 homologue TIP
3	99	94.3	18	AAW37228	p53 N-terminal pep
4	99	94.3	25	AAW54907	Immunodominant epi
5	99	94.3	25	AAW51879	Human p53 amino ac
6	99	94.3	26	AAW60202	p53 peptide used t
7	99	94.3	32	AAW30523	Peptide fragment o
8	99	94.3	36	AAW13604	p53 protein amino
9	99	94.3	41	AAW13603	p53 protein amino
10	99	94.3	52	AAW13602	p53 protein amino

11	99	94.3	64	14	AAW42174	p53 N-terminal fra
12	99	94.3	64	17	AAW07886	Human p53, involv
13	99	94.3	64	19	AAW57240	Human p53 N-termin
14	99	94.3	64	19	AAW48243	Human p53 fragment
15	99	94.3	64	19	AAW42878	N-terminal region
16	99	94.3	64	19	AAW42970	Human MDM2 binding
17	99	94.3	64	20	AAW94303	N-terminal region
18	99	94.3	71	18	AAW47079	Human p53 fragment
19	99	94.3	161	22	AAW36683	Mammalian two-hybr
20	99	94.3	164	22	AAW36689	Mammalian two-hybr
21	99	94.3	211	22	AAW36685	Mammalian two-hybr
22	99	94.3	225	22	AAW36690	Mammalian two-hybr
23	99	94.3	241	15	AAW51872	Human p53 amino ac
24	99	94.3	260	22	ABG03222	Novel human diagno
25	99	94.3	261	21	AAW70714	Human p35 (p53 iso
26	99	94.3	283	22	ABG01512	Novel human diagno
27	99	94.3	337	18	AAW13962	Chimeric p53 prote
28	99	94.3	355	18	AAW13950	Chimeric p53 prote
29	99	94.3	359	18	AAW13960	Del356-393 modifie
30	99	94.3	361	18	AAW13958	Chimeric p53 prote
31	99	94.3	361	18	AAW13961	Chimeric p53 prote
32	99	94.3	363	18	AAW13971	Chimeric p53 prote
33	99	94.3	363	18	AAW13972	Modified p53 varia
34	99	94.3	363	18	AAW13973	Modified p53 varia
35	99	94.3	363	18	AAW13974	Modified p53 varia
36	99	94.3	363	18	AAW13975	Modified p53 varia
37	99	94.3	363	18	AAW13976	Modified p53 varia
38	99	94.3	363	18	AAW13977	Modified p53 varia
39	99	94.3	363	18	AAW13959	Modified p53 varia
40	99	94.3	363	18	AAW13954	Chimeric p53 prote
41	99	94.3	368	18	AAW13956	Chimeric p53 prote
42	99	94.3	370	18	AAW13957	Chimeric p53 prote
43	99	94.3	393	13	AAW22238	Chimeric p53 prote
44	99	94.3	393	13	AAW22238	Sequence of 53 kd
45	99	94.3	393	16	AAW94623	p53. Synthetic.

ALIGNMENTS

RESULT 1
AAW82321
ID AAW82321 standard; Peptide; 19 AA.
XX
AC AAW82321;
XX

22-FEB-1999 (first entry)

p53 homologue TIP peptide.

p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

Synthetic.

WO9847919-A1.

29-OCT-1998.

20-APR-1998; 98WO-GB01140.

22-APR-1997; 97GB-0008089.

(UYDU-) UNIV DUNDEE.

Lane DP;

WPI; 1998-609975/51.

New substance with a mdm2 binding domain and coupling partner

PT useful for stabilising in cells without an efficient mdm2-mediated

degradation pathway

XX

PS Disclosure; Fig 1; 52pp; English.

Wed Feb 12 11:22:44 2003

Best Local Similarity 100.0%; Pred. No. 5.7e-10; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

XX This sequence is a peptide homologue of a region of p53 which binds
CC to mdm2. This peptide is used in the construction of a novel agent
CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
CC production of mdm2 in a population of cells. This agent is also used in
CC the preparation of a therapeutic for activating p53, where the population
CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
CC reducing the clearance of p53 by mdm2, and can be used to activate p53
CC function. The agents for use in therapeutics for activating p53 can be
CC used for the treatment of cancer, viral conditions or other conditions
CC associated with non-functional p53.
XX
XX

SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.7e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPENG 19
Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 2
AAW82319 standard; Peptide; 19 AA.

XX AAW82319;
XX AAW82319;
XX 22-FEB-1999 (first entry)
XX p53 homologue TIP peptide.

XX p53; mdm2; inhibitor; therapy; activator; treatment; cancer; medicament.

XX Synthetic.
XX WO9847525-A1.
XX 29-OCT-1998.

XX 20-APR-1998; 98WO-GB01144.

XX 22-APR-1997; 97GB-0008092.

XX (UYDU-) UNIV DUNDEE.

XX Lane DP;

XX WPI; 1998-609932/51.

XX New agents which inhibit interaction of p53 and mdm2 - useful for
PT activating p53, e.g. for treating cancers, viral conditions or other
PT conditions associated with non functional p53 or mdm2

XX Disclosure; Fig 1; 52pp; English.

XX This sequence is a peptide homologue of a region of p53 which binds
CC to mdm2. This peptide is used in the construction of a novel agent
CC capable of disrupting the binding of p53 and mdm2 or inhibiting the
CC production of mdm2 in a population of cells. This agent is also used in
CC the preparation of a therapeutic for activating p53, where the population
CC of cells do not overexpress mdm2. Inhibiting mdm2 production and/or
CC inhibiting the binding of mdm2 to p53 allows levels of p53 to increase by
CC reducing the clearance of p53 by mdm2, and can be used to activate p53
CC function. The agents for use in therapeutics for activating p53 can be
CC used for the treatment of cancer, viral conditions or other conditions
CC associated with non-functional p53.
XX
XX

SQ Sequence 19 AA;

Query Match 100.0%; Score 105; DB 19; Length 19;

Qy 1 PPLSQETFSDLWKLPPENG 19
Db 1 PPLSQETFSDLWKLPPENG 19

RESULT 3
AAW37228 standard; peptide; 18 AA.

XX AAW37228;

XX 20-JUL-1998 (first entry)

XX p53 N-terminal peptide fragment for Elisa TIP assay.

XX MDM2; oncogenic protein; p53; human; inhibition; interaction; cancer;
KW tumour; diagnosis; binding; viral infection; Elisa TIP assay.

XX Homo sapiens.

XX WO9801467-A2.

XX 15-JAN-1998.

XX 04-JUL-1997; 97WO-EP03549.

XX 07-APR-1997; 97GB-0007041.

XX 05-JUL-1996; 96GB-0014197.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX (NOVS) NOVARTIS AG.

XX Boettger A, Boettger V, Chene P, Furet P, Garcia-scheverria C;

XX Hochkeppel H, Lane D, Picksley S;

XX WPI; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with
PT p53 - useful in, e.g. diagnosis and treatment of cancer and viral
PT infections and identifying binding agents

XX Disclosure; Page 34; 45pp; English.

XX This represents a p53 N-terminal peptide fragment used in an Elisa TIP
CC assay for analysing the interaction between human oncogenic protein MDM2
CC and p53. The invention provides peptide derivatives capable of binding to
CC the human MDM2. These peptides can specifically inhibit or block the
CC binding of MDM2 to the human p53 protein, in vitro or in vivo. Inhibiting
CC the interaction between the p53 and MDM2 can induce growth arrest or
CC apoptosis in tumour cells comprising a wild-type p53 and non-elevated
CC levels of MDM2. The peptides may be used to identify molecules that bind
CC to MDM2 and to identify and design inhibitors of MDM2/p53 binding. They
CC may also be used to purify binding partners especially MDM2, diagnose
CC disease by measuring levels of MDM2 in blood of cancer and leukaemia
CC patients and for treatment or prevention of disease involving p53/MDM2
CC interactions, especially tumours and viral infections. The peptides can
CC be administered nasally, rectally, orally or by injection. By interfering
CC with MDM2/p53 interaction, the peptides can activate p53 function and
CC accumulation in normal cells. The peptides which mimic the MDM2 binding
CC site in p53, have a significantly greater blocking activity compared
CC with wild-type p53.

XX Sequence 18 AA;

Query Match 94.3%; Score 99; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.9e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPPEN 18

Db 1 PPLSQETFSDLWKLLPEN 18

RESULT 4

ID AAR54907 standard; peptide; 25 AA.

XX AC AAR54907;

XX DT 29-NOV-1994 (first entry)

XX DE Immunodominant epitope from p53 N-terminal.

XX KW cancer; pre-cancerous state; detection; diagnosis; human p53 gene;

XX KW immunodominant epitope; human cellular tumour antigen;

XX KW transformation-associated protein.

XX OS Homo sapiens.

XX PN WO9410306-A.

PD 11-MAY-1994.

PF 02-NOV-1993; 93WO-FR01082.

PR 02-NOV-1992; 92FR-0013110.

XX PA (EURO-) LAB EURO BIO SA.

XX PI Legros Y, Lubin R, Soussi T;

XX DR WPI; 1994-167463/20.

XX PT New immuno:dominant epitope(s) of protein p53 - for detecting and

XX PT monitoring antibodies indicative of cancer and precancerous

XX PS Claim 4; Page 42; 62pp; French.

XX CC Peptides derived from the N-terminal (amino acids 1-112) or the C-terminal (amino acids 350-393) of protein p53 which specifically react with anti-p53 antibodies in patients with cancer or precancerous conditions are claimed. The peptides (AAR54907-R54921) are useful for detecting and monitoring cancerous and precancerous conditions.

SQ Sequence 25 AA;

Query Match

Best Local Similarity 94.3%; Score 99; DB 15; Length 25;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 2 PPLSQETFSDLWKLLPEN 19

RESULT 5

AAR51879

ID AAR51879 standard; Protein; 25 AA.

XX AC AAR51879;

XX DT 18-NOV-1994 (first entry)

XX DE Human p53 amino acids 9-33.

XX KW Human nuclear phosphoprotein p53; tumour suppressor gene product;

XX KW anti-oncogene; cancer; tumour; antibody binding region; epitope.

XX OS Homo sapiens.

XX PN WO9408241-A.

XX PD

XX PF 14-APR-1994.

XX PR 30-SEP-1993; 93WO-EP02666.

XX PR 30-SEP-1992; 92DE-4232823.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.

XX PI Klein R, Schranz P, Tessmer C, Volkmann M, Zentgraf H;

XX DR WPI; 1994-135732/16.

XX DR N-PSDB; AAQ62365.

XX PT Non-radioactive detection of p53 specific antibodies - by capture on immobilised p53 or its fragments, then reaction with labelled second antibody, for diagnosis of tumours and suitable for screening

XX PS Claim 11; Page 19; 35pp; German.

XX CC Antibodies specific for p53 are detected by binding to immobilised fragments of the p53 gene product containing the antibody-binding region. Preferred fragments contain amino acids 1-241, 40-349, 40-393, 66-241, 66-393, 237-349, 237-393 and esp. 9-33, 37-52 or 368-386. See AAR51872-R51881 for sequences of these fragments.

XX SQ Sequence 25 AA;

Query Match

Best Local Similarity 94.3%; Score 99; DB 15; Length 25;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 4 PPLSQETFSDLWKLLPEN 21

RESULT 6

AAW60202

ID AAW60202 standard; peptide; 26 AA.

XX AC AAW60202;

XX DT 18-AUG-1998 (first entry)

XX DE p53 peptide used to detect antibodies against p53.

XX KW Human; p53; antibody; detection; biosensor; cancer patient;

XX KW p53 gene therapy; immune response; mutant.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9815834-A1.

XX PD 16-APR-1998.

XX PF 01-OCT-1997; 97WO-US16132.

XX PR 07-OCT-1996; 96US-0028533.

XX PA (SCHE) SCHERING CORP.

XX PI Mytych DT, Swanson SJ;

XX WPI; 1998-240965/21.

XX DR Detecting antibodies that bind p53 by reaction with immobilised p53 peptide(s) - attached directly to flow cells in the sensor chip of bio-sensor, used to analyse serum from cancer patients, e.g. those being given p53 gene therapy

Wed Feb 12 11:22:44 2003

PS Claim 4; Page 5; 41pp; English.
 CC Peptides AAW60202-05 are derived from human p53 protein. The present
 CC peptide corresponds to residues 11-35. The peptides are used in
 CC the method of the invention. Antibodies that bind to p53 protein are
 CC detected by immobilising a p53 peptide directly on to a flow cell of
 CC a sensor chip in a biosensor, treating the peptide with a sample of
 CC patient serum, diluted in buffer, and measuring binding of antibody
 CC to the peptide using the biosensor. The method is used to monitor
 CC cancer patients undergoing p53 gene therapy (to determine if an
 CC immune response has developed), and also to detect antibodies against
 CC mutant forms of p53.

XX SQ Sequence 26 AA;
 Query Match 94.3%; Score 99; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 7.4e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 3 PPLSQETFSDLWKLLPEN 20

RESULT 7
 AAB30523
 ID AAB30523 standard; peptide; 32 AA.
 AC AAB30523;
 DT 06-MAR-2001 (first entry)

XX Peptide fragment of a tumour suppressor protein p53.
 DE Biologically active compound; cellular metabolism; DNA replication;
 KW RNA transcription; RNA translation; RNA elongation; RNA processing;
 KW protein synthesis; protein processing; cellular differentiation;
 KW cell division; ion channel transmission; cellular protein; toxin;
 KW RNA transportation; cellular oxidation; tumour suppressor p53;
 KW plasmidogen antigen activator.

XX Synthetic.
 OS WO200061775-A1.
 PN 19-OCT-2000.
 PD 08-APR-1999; 99WO-IB00616.
 PF 08-APR-1999; 99WO-IB00616.
 PR (SERG/) SERGEEV P.
 PA Sergeev P;
 PI WPI; 2001-006911/01.

XX Novel methods for the synthesis of biologically active compounds from
 XX inactive precursors in the cells of living organisms, useful for
 XX producing proteins or polynucleotides -
 XX Example 8; Page 29; 65pp; English.
 CC The specification describes a method of synthesis of biologically active
 CC substances of determined structure directly in the cells of living
 CC organisms containing specific RNA or DNA sequence. The method is based
 CC on the hybridisation of two or more oligomers bound with biologically
 CC inactive substances to specific RNA or DNA in vivo in the cells of
 CC living organisms. After hybridisation of the oligomers, the biologically
 CC inactive precursors bound to the oligomers can interact with each other
 CC to make the active form of the substances. This changing of properties
 CC is due to chemical reactions which bind the biologically inactive
 CC precursors through a chemical bond into a biologically active form of

the whole compound. The methods are useful for producing biologically
 active compounds from inactive precursors. These compounds may be
 inhibitors or stimulators of cellular metabolism, DNA replication, RNA
 transcription, RNA translation, RNA elongation RNA processing, protein
 synthesis, protein processing, cellular differentiation, cell division,
 ion channel transmission, cellular protein and RNA transportation,
 processes of cellular oxidation, toxins, proteins or RNAs. AAB30523-36
 represent peptides which are bound to oligomers AAC62167-80 and
 AAC62181-94. The peptides are fragments of the tumour suppressor p53, and
 the oligomers are antiparallel to human plasmidogen antigen activator
 mRNA (AAC62167-80) or human NHO1 (AAC62181-94). The method of the
 invention is used to produce the tumour suppressor protein p53 from the
 bound peptides and oligomers.

XX SQ Sequence 32 AA;
 Query Match 94.3%; Score 99; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 8
 AAW13604
 ID AAW13604 standard; peptide; 36 AA.
 AC AAW13604;
 DT 16-JAN-1998 (first entry)

XX p53 protein amino acids 6-41.
 DE Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
 KW restenosis.

XX Homo sapiens.
 OS WO9709343-A2.
 PN 13-MAR-1997.
 PD 02-SEP-1996; 96WO-FR01340.
 PF 04-SEP-1995; 95FR-0010331.
 PR (INRM) INST NAT SANTE & RECH MEDICALE.
 PA (RHON) RHONE POULENC RORER SA.
 PI Dubs-Poterszman M, Tocque B, Wasylyk B;
 XX WPI; 1997-192837/17.

XX Treating cancer with antagonist of oncogenic activity of protein
 XX Mdm2 - or nucleic acid encoding an antagonist, also viral vectors
 XX contg. this nucleic acid
 XX Claim 4; Page -; 43pp; French.
 CC The peptides AAW13602-6 represent peptide fragments derived from the
 CC wild type human p53 protein. This peptide corresponds to amino acids
 CC 6-41 of the p53 sequence. The peptides are claimed peptides which are
 CC able to bind the N-terminal amino acids (1-134) of the murine double
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD
 CC phosphoprotein which binds and modulates the activity of the tumour
 CC suppressor protein p53. It has now been shown that the mdm2 protein
 CC itself has oncogenic properties, especially in a p53-null background.
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by

CC over-expression of the p107 protein. The p53 peptides are examples of
 CC antagonists of the invention which are able to inhibit the oncogenic
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B
 CC cell lymphoma, or other hyperproliferative conditions such as
 CC restenosis. Note: this sequence is not given in the specification but is
 CC constructed from the wild type human p53 sequence.

XX Sequence 36 AA;

Query Match 94.3%; Score 99; DB 18; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 7 PPLSQETFSDLWKLLPEN 24

RESULT 9

AAW13603
 ID AAW13603 standard; peptide; 41 AA.

XX AC AAW13603;

DT 16-JAN-1998 (first entry)

DE p53 protein amino acids 1-41.

XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
 KW restenosis.

XX Homo sapiens.

XX WO9709343-A2.

PN 13-MAR-1997.

XX 02-SEP-1996; 96WO-FR01340.

XX 04-SEP-1995; 95FR-0010331.

XX (INRM) INST NAT SANTE & RECH MEDICALE.
 XX (RHON) RHONE POULENC RORER SA.

PI Dubs-Poterszman M, Tocque B, Wasylyk B;

XX WPI; 1997-192837/17.

XX Treating cancer with antagonist of oncogenic activity of protein
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors
 PT contg. this nucleic acid

PS Claim 4; Page -; 43pp; French.

XX The peptides AAW13602-6 represent peptide fragments derived from the
 CC wild type human p53 protein. This peptide corresponds to amino acids
 CC 1-41 of the p53 sequence. The peptides are claimed peptides which are
 CC able to bind the N-terminal amino acids (1-134) of the murine double
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD
 CC phosphoprotein which binds and modulates the activity of the tumour
 CC suppressor protein p53. It has now been shown that the mdm2 protein
 CC itself has oncogenic properties, especially in a p53-null background.
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by
 CC over-expression of the p107 protein. The p53 peptides are examples of
 CC antagonists of the invention which are able to inhibit the oncogenic
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B
 CC cell lymphoma, or other hyperproliferative conditions such as
 CC restenosis. Note: this sequence is not given in the specification but is

CC constructed from the wild type human p53 sequence.

XX Sequence 41 AA;

Query Match 94.3%; Score 99; DB 18; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 10

AAW13602

ID AAW13602 standard; peptide; 52 AA.

XX AC AAW13602;

DT 16-JAN-1998 (first entry)

DE p53 protein amino acids 1-52.

XX Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
 KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
 KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
 KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
 KW restenosis.

XX Homo sapiens.

XX WO9709343-A2.

PN 13-MAR-1997.

XX 02-SEP-1996; 96WO-FR01340.

XX 04-SEP-1995; 95FR-0010331.

XX (INRM) INST NAT SANTE & RECH MEDICALE.
 XX (RHON) RHONE POULENC RORER SA.

PI Dubs-Poterszman M, Tocque B, Wasylyk B;

XX WPI; 1997-192837/17.

XX Treating cancer with antagonist of oncogenic activity of protein
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors
 PT contg. this nucleic acid

PS Claim 4; Page -; 43pp; French.

XX The peptides AAW13602-6 represent peptide fragments derived from the
 CC wild type human p53 protein. This peptide corresponds to amino acids
 CC 1-52 of the p53 sequence. The peptides are claimed peptides which are
 CC able to bind the N-terminal amino acids (1-134) of the murine double
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD
 CC phosphoprotein which binds and modulates the activity of the tumour
 CC suppressor protein p53. It has now been shown that the mdm2 protein
 CC itself has oncogenic properties, especially in a p53-null background.
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by
 CC over-expression of the p107 protein. The p53 peptides are examples of
 CC antagonists of the invention which are able to inhibit the oncogenic
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B
 CC cell lymphoma, or other hyperproliferative conditions such as
 CC restenosis. Note: this sequence is not given in the specification but is
 CC constructed from the wild type human p53 sequence.

XX Sequence 52 AA;

Query Match 94.3%; Score 99; DB 18; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 PPLSQETFSDLWKLLPEN 18
Db	12 PPLSQETFSDLWKLLPEN 29
RESULT 11	
AAR42174	
ID	AAR42174 standard; peptide; 64 AA.
AC	AAW07886;
AC	AAR42174;
XX	28-JAN-1997 (first entry)
XX	Human p53, involved in tumour suppression.
XX	p53; MDM-2; binding-inhibitor; identification; tumour; cancer;
XX	neoplasia; antibody fusion protein; therapy.
XX	Homo sapiens.
XX	Key
XX	Region 1..41
XX	/note= "MDM-2 binding fragment"
XX	Region 1..50
XX	/note= "MDM-2 binding fragment"
XX	Region 13..57
XX	/note= "MDM-2 binding fragment"
XX	US5550023-A.
XX	27-AUG-1996.
XX	07-APR-1992; 92US-0867840.
XX	07-APR-1993; 93US-0044619.
XX	07-APR-1992; 92US-0867840.
XX	23-JUN-1992; 92US-0903103.
XX	18-MAY-1994; 94US-0245500.
XX	(UYJO) UNIV JOHNS HOPKINS.
XX	Kinzler KW, Vogelstein B;
XX	WPI; 1996-401591/40.
XX	Identification of cpds. interfering with human MDM2/p53 binding -
XX	useful as therapeutic agents to treat human neoplastic cells
XX	Claim 16; Column 19-20; 36pp; English.
XX	AAW07886 represents the human p53 protein which is involved in the
XX	development of many cancers. The protein is used here in a method
XX	for identifying compounds that interfere with the binding of p53 and
XX	MDM-2. In binding the p53 protein, the MDM-2 protein releases a cell
XX	from p53-regulated growth, allowing cancers to develop. Therefore
XX	compounds identified as interfering with the binding of MDM-2 to p53
XX	are potentially useful in the treatment of human neoplastic cells. In
XX	the method pref. one or both of the proteins is a fusion protein esp.
XX	with an antibody or antibody fragment which aids separation and
XX	identification.
XX	Sequence 64 AA;
XX	Query Match 94.3%; Score 99; DB 17; Length 64;
XX	Best Local Similarity 100.0%; Pred. No. 2e-08;
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 PPLSQETFSDLWKLLPEN 18
Db	12 PPLSQETFSDLWKLLPEN 29
RESULT 13	
AAW57240	
ID	AAW57240 standard; protein; 64 AA.
AC	AAW57240;
XX	10-AUG-1998 (first entry)
XX	Human p53 N-terminal fragment.

XX Human; p53; MDM2; tumour; growth inhibition; amplification;
 KW malignant fibrous histiocytoma; liposarcoma.
 XX

OS Homo sapiens.

XX US5756455-A.

XX 26-MAY-1998.

XX 17-FEB-1995; 95US-0390515.

XX 07-APR-1993; 93US-0044619.

XX 07-APR-1992; 92US-0867840.

XX 23-JUN-1992; 92US-0903103.

XX 17-FEB-1995; 95US-0390515.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Kinzler KW, Vogelstein B;

XX WPI; 1998-321574/28.

XX Inhibiting growth of tumour cells having MDM2 gene amplification -

XX with p53 protein fragment

XX Claim 1; Column 19-20; 40pp; English.

XX A method has been developed for inhibiting the growth of tumour cells
 CC containing a human MDM2 gene amplification. The method comprises
 CC treating the tumour cells with a DNA molecule that expresses a
 CC polypeptide capable of binding to human MDM2 protein. The present
 CC sequence represents an N-terminal fragment of p53 which can bind to the
 CC human MDM2 protein. The present invention describes three preferred
 CC polypeptides for binding human MDM2: (1) the polypeptide comprises
 CC amino acids 1-50 of p53 (see AAW57240); (2) the polypeptide comprises
 CC amino acids 13-41 of p53 (see AAW57240); and at least one additional p53
 CC residues on the N- or C-terminal side, provided that the polypeptide
 CC lacks the homooligomerisation domain of p53; (3) the polypeptide
 CC comprises amino acids 13-41 of p53 (see AAW57241) and at least nine
 CC additional p53 residues on the N- or C-terminal side, provided that the
 CC polypeptide lacks amino acids 138-393 of p53. Some malignant fibrous
 CC histiocytomas and liposarcomas have an MDM2 gene amplification, so
 CC detection of increased expression of MDM2 gene products indicates
 CC tumorigenesis.
 XX

XX Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 14

AAW48243

ID AAW48243 standard; peptide; 64 AA.

XX AAW48243;

XX 18-JUN-1998 (first entry)

XX Human p53 fragment 13-41.

XX Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease; p53;
 KW sarcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma.
 XX

OS Homo sapiens.

XX US5736338-A.

XX

XX 07-APR-1998.

XX 17-FEB-1995; 95US-0390517.

XX 07-APR-1993; 93US-0044619.

XX 07-APR-1992; 92US-0867840.

XX 23-JUN-1992; 92US-0903103.

XX 17-FEB-1995; 95US-0390517.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX WPI; 1998-239206/21.

XX Cancer diagnosis - by determination of MDM2 protein

XX Disclosure; Column 19-20; 35pp; English.

XX The present sequence represents a human p53 fragment 13-41 which is

XX necessary for the interaction of MDM-2 and p53. The present invention

XX describes a method for diagnosing a neoplastic disease caused by

XX overexpression of MDM2 protein. The method comprises detecting an

XX elevated cellular amount of this protein. The method is useful for the

XX diagnosis of sarcoma, especially liposarcoma, malignant fibrous

XX histiocytoma or osteosarcoma.

XX SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 15

AAW42878

ID AAW42878 standard; Protein; 64 AA.

XX AAW42878;

XX 30-APR-1998 (first entry)

XX N-terminal region of p53 (amino acids 13-41).

XX MDM2; tumour; diagnosis; neoplasia; DNA binding protein;

XX p53 polypeptide; binding; tumour cell; p53-regulated growth;

XX inhibition; anti-cancer agent.

XX Homo sapiens.

XX US5708136-A.

XX 13-JAN-1998.

XX 17-FEB-1995; 95US-0390516.

XX 07-APR-1993; 93US-0044619.

XX 07-APR-1992; 92US-0867840.

XX 23-JUN-1992; 92US-0903103.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX WPI; 1998-100408/09.

XX Human MDM2 binding polypeptide - comprises fragments of p53, useful

XX in re-establishing p53-regulated growth control in cells

XX PT

PT over-expressing MDM2

XX Claim 1; Columns 19-20; 41pp; English.

XX The present sequence represents a N-terminal portion of the p53 protein.
 CC These amino acid residues have been found to be necessary for the
 CC interaction of MDM2 and p53. A cell containing three recombinant
 CC DNA constructs was produced. These constructs encode an MDM2 protein
 CC fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 CC to a transcriptional activation domain, and a reporter gene downstream
 CC from a DNA element which is recognised by the sequence-specific
 CC DNA-binding domain. The cell is used to identify a compound which
 CC interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed
 CC in tumour cells and since binding of MDM2 to p53 appears to allow tumour
 CC cells to escape from p53-regulated growth, compounds that inhibit such
 CC binding would be useful as anti-cancer agents.

XX SQ Sequence 64 AA;

Query Match 94.3%; Score 99; DB 19; Length 64;

Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

Search completed: February 12, 2003, 10:34:44
 Job time : 37 secs

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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:33:46 ; Search time 15 seconds
(without alignments)
121.770 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	94.3	391	2 JC6193	tumor suppressor p
2	99	94.3	393	1 DNHU53	cellular tumor ant
3	99	94.3	393	1 S06594	cellular tumor ant
4	94	89.5	386	1 S51648	cellular tumor ant
5	86	81.9	393	2 JC6176	tumor suppressor p
6	86	81.9	396	1 JH0633	cellular tumor ant
7	81	77.1	363	1 A29376	cellular tumor ant
8	74	70.5	381	2 S38824	cellular tumor ant
9	74	70.5	390	1 DNWS53	cellular tumor ant
10	72	68.6	391	1 S02192	cellular tumor ant
11	60	57.1	396	1 JH0631	cellular tumor ant
12	51.5	49.0	1009	2 S28857	glutamate receptor
13	51.5	49.0	1009	2 JH0266	glutamate receptor
14	50	47.6	230	2 C64396	precorrin-2 methyl
15	50	47.6	367	2 G86715	racemase [imported
16	50	47.6	447	2 E96672	Similar to Flavono
17	48	45.7	119	2 C49921	major intracellular
18	48	45.7	308	2 AD3262	methylntransferase
19	48	45.7	1004	2 B25039	outer cell wall pr
20	47	44.8	157	1 VCTMPV	coat protein - pep
21	47	44.8	469	2 G84779	hypothetical prote
22	47	44.8	487	2 D83027	hypothetical prote
23	47	44.8	489	2 T41241	oxysterol-binding
24	47	44.8	956	2 G70327	isoleucine-tRNA li
25	46.5	44.3	250	2 T01604	hypothetical prote
26	46.5	44.3	485	2 C75460	hypothetical prote
27	46	43.8	274	2 S74792	hypothetical prote
28	46	43.8	293	1 D69300	4-hydroxybenzoate
29	45.5	43.3	250	2 T49221	hypothetical prote

30 45 42.9 367 2 B96796 hypothetical prote
31 45 42.9 405 2 AD2194 hypothetical prote
32 45 42.9 837 2 I57557 DNA-binding protei
33 44.5 42.4 211 2 B95064 conserved hypotHet
34 44.5 42.4 211 2 D97931 conserved hypotHet
35 44 41.9 113 1 F3WLB4 L3 protein - bovin
36 44 41.9 114 2 S03072 L3 protein - bovin
37 44 41.9 134 2 A82749 hypothetical prote
38 44 41.9 209 2 S61204 hypothetical prote
39 44 41.9 211 1 ASLJM5 NEF protein - simi
40 44 41.9 238 2 S61205 NEF protein - simi
41 44 41.9 239 2 S54852 NEF protein - simi
42 44 41.9 244 2 S61206 NEF protein - simi
43 44 41.9 244 2 S61208 NEF protein - simi
44 44 41.9 246 2 S54853 NEF protein - simi
45 44 41.9 250 2 S54849 nef protein - simi

ALIGNMENTS

RESULT 1

JC6193

tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC6193

R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; MUID:97208869; PMID:9055811

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: EMBL:X90592; NID:gl532043; PIDN:CAA62216.1; PID:gl532044

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match 94.3%; Score 99; DB 2; Length 391;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 2

DNHU53

cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor

C:Species: Homo sapiens (man)

C>Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000

C:Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397; S42

4905; I58354; I78850; I52681; S60153

R:Lamb, P.; Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416; PMID:2946935

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LAM>

A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:gl89460; PIDN:AAAS9987.1; PID

F:Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A:Title: A variation in the structure of the protein-coding region of the human p53 gene

A:Reference number: JT0436; MUID:89108008; PMID:2905688

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUCL>

A:Cross-references: EMBL:M22898; NID:gl89474

A;Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele
A;Accession: J0436
A;Molecule type: DNA
A;Residues: 1-71,'P',73-393 <BUC2>
A;Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476
A;Note: this 72-Pro allele was found in both normal and malignant cell lines
R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
A;Reference number: S40773
A;Accession: S40773
A;Molecule type: DNA
A;Residues: 1-393 <CHU>
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
EMBO J. 3, 3257-3262, 1984
A;Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 cDNA clone in COS cells
A;Reference number: S42669; MUID:85126934; PMID:6396087
A;Accession: S42669
A;Molecule type: mRNA
A;Residues: 101-393 <MKI1>
A;Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241
R;Zakut-Houri, R.; Bien-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A;Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
A;Reference number: A22837; MUID:85230577; PMID:4006916
A;Accession: A22837
A;Molecule type: mRNA
A;Residues: 1-71,'P',73-393 <ZAK>
A;Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
A;Molecule type: mRNA
A;Residues: 1-71,'P',73-272,'H',274-393 <HAR>
A;Cross-references: GB:X03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
R;Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A;Title: Molecular basis for heterogeneity of the human p53 protein.
A;Reference number: A93086; MUID:87089826; PMID:3025664
A;Accession: A25397
A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A;Accession: B25397
A;Molecule type: mRNA
A;Residues: 1-71,'P',73-78,'T',80-393 <HAR2>
A;Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A;Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A;Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A;Reference number: S42452; MUID:87144273; PMID:3547088
A;Accession: S42452
A;Molecule type: mRNA; DNA
A;Residues: 66-71,'P',73-79 <MKI2>
A;Experimental source: clone lambda C113
A;Note: 72-Cys was also found, and appears to represent a polymorphism
A;Accession: S42453
A;Molecule type: mRNA; DNA
A;Residues: 66-79 <MKI3>
A;Experimental source: clone J6K
R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
EMBO J. 10, 2879-2887, 1991
A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A;Reference number: I38082; MUID:92007731; PMID:1315267
A;Accession: I38082
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-389,'LLSILSEWKEICWSIWNTEITLFDIIVWCPMSRLRLALT','VPPSTTTTCVTPAWAA' <F01>

A;Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A;Note: deletion of a C nucleotide causes a frameshift at position 566
A;Accession: I38083
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-192,'R',194-393 <F02>
A;Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
A;Accession: I38084
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-393 <F03>
A;Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437
A;Accession: I38085
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-245,'T',247-393 <F04>
A;Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439
A;Accession: I38086
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-236,'I',238-393 <F05>
A;Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
A;Accession: I38087
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F06>
A;Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
A;Accession: I38088
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-71,'P',73-237,'Y',239-393 <F07>
A;Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
A;Accession: I38089
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F08>
A;Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A;Accession: I38090
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-71,'P',73-162,'H',164-393 <F09>
A;Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449
A;Accession: I38091
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212,'Q',214-393 <F10>
A;Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A;Accession: I38092
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-253,'D',255-393 <F11>
A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A;Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A;Title: An Alu polymorphism intragenic to the TP53 gene.
A;Reference number: I38093; MUID:92107726; PMID:1762941
A;Accession: I38093
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393 <FUT>
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani
Cancer Res. 51, 5800-5805, 1991
A;Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell lines
A;Reference number: A44905; MUID:92034678; PMID:1933850
A;Accession: A44905
A;Molecule type: DNA
A;Residues: 246-247,'W',249-250 <YAM>
A;Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830
A;Note: sequence extracted from NCBI backbone (NCBI:63157, NCBI:63159)
A;Note: mutation from a liver metastasis of a gastric cancer
R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.

Oncogene 6', 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: I58354; MUID:91296386; PMID:1648702
 A:Accession: I58354
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:gl679931; PIDN:AAB19324.1; PID:g232814
 A:Accession: I78850
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-references: GB:S41977; NID:gl679932; PIDN:AAB19325.1; PID:g232816
 R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphobla
 A:Reference number: I52681; MUID:94036762; PMID:8221626
 A:Accession: I52681
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'DOTSFQKENC' <CHO>
 A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
 A>Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymph
 R:Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
 A:Reference number: S60151; MUID:96133682; PMID:8552047
 A:Accession: S60151
 A:Molecule type: DNA
 A:Residues: 3-44 <PET>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, p53, HSP70,

Query Match 94.3%; Score 99; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLEN 29

RESULT 3
 cellular tumor antigen p53 - green monkey
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S06594
 R:Rigaudy, P.; Eckhart, W.
 Nucleic Acids Res. 17, 8375, 1989
 A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.
 A:Reference number: S06594; MUID:90045967; PMID:2530498
 A:Accession: S06594
 A:Molecule type: mRNA
 A:Residues: 1-393 <RIG>
 A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
 F:176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 94.3%; Score 99; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLEN 29

RESULT 4
 S51648

cellular tumor antigen p53 - bovine
 N:Alternate names: tumor-suppressor protein p53
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S51648
 R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.
 submitted to the EMBL Data Library, September 1994
 A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its
 A:Reference number: S51648
 A:Accession: S51648
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-396 <DEQ>
 A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein
 F:168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 89.5%; Score 94; DB 1; Length 386;
 Best Local Similarity 94.4%; Pred. No. 1.7e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLEN 29

RESULT 5
 JC6176
 tumor suppressor protein p53 - Chinese hamster
 C:Species: Cricetulus griseus (Chinese hamster)
 C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
 C:Accession: JC6176
 R:Lee, H.; Larner, J.M.; Hamlin, J.L.
 Gene 184, 177-183, 1997
 A:Title: Cloning and characterization of Chinese hamster p53 cDNA.
 A:Reference number: JC6176; MUID:97183659; PMID:9031625
 A:Contents: liver
 A:Accession: JC6176
 A:Molecule type: mRNA
 A:Residues: 1-393 <LEE>
 A:Cross-references: GB:U050395; NID:gl842229; PIDN:AAC53040.1; PID:gl842230
 C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
 iption, and recombination by protein/protein interactions.
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: liver; tumor

Query Match 81.9%; Score 86; DB 2; Length 393;
 Best Local Similarity 94.1%; Pred. No. 2.8e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLLEN 18
 |||||
 Db 13 PLSQETFSDLWKLLEN 29

RESULT 6
 JH0633
 cellular tumor antigen p53 - golden hamster
 N:Alternate names: tumor-suppressor protein p53
 C:Species: Mesocricetus auratus (golden hamster)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0633
 R:Legros, Y.; McIntyre, P.; Soussi, T.
 Gene 112, 247-250, 1992
 A:Title: The cDNA cloning and immunological characterization of hamster p53.
 A:Reference number: JH0633; MUID:92210007; PMID:1555773
 A:Accession: JH0633
 A:Molecule type: mRNA
 A:Residues: 1-396 <LEG>

A;Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
 A;Experimental source: kidney, strain MP1
 C;Genetics:

A;Gene: p53
 C;Superfamily: cellular tumor antigen p53
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
 F;119,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
 F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 81.9%; Score 86; DB 1; Length 396;
 Best Local Similarity 94.1%; Pred. No. 2.9e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLPPN 18
 |||||
 Db 13 PLSQETFSDLWKLPPN 29

RESULT 7

A29376
 C;Superfamily: cellular tumor antigen p53 - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A29376; S61531; S72313; I51639
 R;Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
 Oncogene 1, 71-78, 1987

A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein

A;Reference number: A29376; MUID:88143684; PMID:2830576

A;Accession: A29376

A;Molecule type: mRNA

A;Residues: 1-363 <SOU>

A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962

R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A;Title: Overexpression of wild-type p53 interferes with normal development in Xenopus 1

A;Reference number: I51639; MUID:94134403; PMID:8302570

A;Accession: S61531

A;Molecule type: mRNA

A;Residues: 1-293,295-363 <HOE>

A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.

submitted to the EMBL Data Library, March 1994

A;Reference number: S72313

A;Accession: S72313

A;Molecule type: mRNA

A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>

A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514

C;Genetics:

A;Gene: p53

C;Superfamily: cellular tumor antigen p53

C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph

F;150,153,213,217/Binding site: zinc (Cys, His, Cys) #status predicted

F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

77.1%; Score 81; DB 1; Length 363;

Best Local Similarity 82.4%; Pred. No. 0.00015;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLPE 17
 |||||
 Db 11 PPLSQETFSDLWKLPE 27

RESULT 8

S38824

C;Superfamily: cellular tumor antigen p53, minor splice form - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S38824; S35478

R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986

A;Title: Immunologically distinct p53 molecules generated by alternative splicing.

A;Reference number: S38822; MUID:87064640; PMID:3023970

A;Accession: S38824

A;Molecule type: mRNA

A;Residues: 1-381 <ARA>

A;Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

R;Han, K.A.; Kulesz-Martin, M.F.

Nucleic Acids Res. 20, 1979-1981, 1992

A;Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss

A;Reference number: S35478; MUID:92253421; PMID:1579500

A;Accession: S35478

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-381 <HAN>

A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988

C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks th

s not known.

C;Superfamily: cellular tumor antigen p53

C;Keywords: alternative splicing; phosphoprotein; zinc

F;1-44/Domain: transcription activation #status predicted <TRA>

F;16-26/Region: conserved region I

F;99-289/Domain: DNA-binding core #status predicted <DBC>

F;108-121/Region: L1 loop

F;114-139/Region: conserved region II

F;160-192/Region: L2 loop

F;168-178/Region: conserved region III

F;231-252/Region: conserved region IV

F;267-283/Region: conserved region V

F;313-319/Region: nuclear location signal

F;319-357/Region: tetramer association

F;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted

F;173,176,235,239/Binding site: zinc (Cys, His, Cys) #status predicted

F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match

70.5%; Score 74; DB 2; Length 381;

Best Local Similarity 93.3%; Pred. No. 0.0018;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PLSQETFSDLWKLPP 16
 |||||
 Db 16 PLSQETFSGLWKLPP 30

RESULT 9

DNMS53

C;Superfamily: cellular tumor antigen p53 - mouse

N;Alternate names: oncoprotein p53

C;Species: Mus musculus (house mouse)

C;Date: 28-Aug-1985 #sequence revision 04-Oct-1996 #text_change 11-May-2000

C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703

R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.

EMBO J. 3, 2179-2183, 1984

A;Title: Analysis of the gene coding for the murine cellular tumour antigen p53.

A;Reference number: A22739; MUID:85027173; PMID:6092064

A;Accession: A22739

A;Molecule type: DNA

A;Residues: 1-134,'V',136-390 <BIE>

A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237; GB

R;Chumakov, P.M.

Bioorg. Khim. 13, 1691-1694, 1987

A;Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.

A;Reference number: S06336; MUID:88221682; PMID:3329909

A;Accession: S06336

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-134,'V',136-390 <CHU>

R;Zakut-Houri, R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D.

Nature 306, 594-597, 1983

A;Title: A single gene and a pseudogene for the cellular tumour antigen p53.

A;Reference number: A02684; MUID:84068204; PMID:6646235

A;Accession: A02684

A;Molecule type: mRNA

A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>

Wed Feb 12 11:22:49 2003

A;Cross-references: GB:X01237; GB:K01700; NID:g53575
 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A;Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A;Reference number: S38822; MUID:87064640; PMID:3023970
 A;Accession: S38822
 A;Molecule type: mRNA
 A;Residues: 1-390 <ARA2>
 A;Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
 A;Accession: S38823
 A;Molecule type: mRNA
 A;Residues: 1-167, 'G', '169-233', 'I', '235-390 <ARA2>
 A;Cross-references: EMBL:M13873
 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Submitted to the EMBL Data Library, July 1988
 A;Reference number: S40014
 A;Accession: S40014
 A;Molecule type: mRNA
 A;Residues: 1-167, 'G', '169-390 <ARA3>
 A;Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201
 R;Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
 Nucleic Acids Res. 12, 5609-5626, 1984
 A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the
 A;Reference number: I48703; MUID:84272240; PMID:6379601
 A;Accession: I48703
 A;Status: translated from GB/EMBL/DB3
 A;Molecule type: mRNA
 A;Residues: 1-47, 'R', '49-78', 'QW', '82-390 <RES>
 A;Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
 C;Comment: This DNA-binding protein plays an essential role in the regulation of cell di
 C;Superfamily: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-tu
 C;Comment: cellular tumor antigen p53
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
 F;1-44/Domain: transcription activation #status predicted <TRA>
 F;16-26/Region: conserved region I
 F;99-289/Domain: DNA-binding core #status predicted <DBC>
 F;108-121/Region: L1 loop
 F;114-139/Region: conserved region II
 F;160-192/Region: L2 loop
 F;168-178/Region: conserved region III
 F;231-252/Region: conserved region IV
 F;233-248/Region: L3 loop
 F;267-283/Region: conserved region V
 F;313-319/Region: nuclear location signal
 F;319-357/Region: tetramer association
 F;7-9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F;7-9,12,18,23,37/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
 F;389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 70.5%; Score 74; DB 1; Length 390;
 Best Local Similarity 93.3%; Pred. No. 0.0018;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16
 |||||
 Db 16 PLSQETFSGLWKLLP 30

RESULT 10
 S02192
 cellular tumor antigen p53 - rat
 N;Alternate names: gene p53 protein; nuclear oncoprotein p53
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: S02192; S41149
 R;Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
 Nucleic Acids Res. 16, 11384, 1988
 A;Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
 A;Reference number: S02192; MUID:89083585; PMID:3060862
 A;Accession: S02192
 A;Molecule type: mRNA
 A;Residues: 1-391 <SOU>

A;Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
 R;Hulla, J.E.; Schneider, R.P.
 Nucleic Acids Res. 21, 713-717, 1993
 A;Title: Structure of the rat p53 tumor suppressor gene.
 A;Reference number: S41149; MUID:93181268; PMID:8441680
 A;Accession: S41149
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-173, 'W', '175-391 <HUL>
 A;Cross-references: EMBL:L07909
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
 C;Genetics:
 A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
 C;Superfamily: cellular tumor antigen p53
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
 F;174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 68.6%; Score 72; DB 1; Length 391;
 Best Local Similarity 93.3%; Pred. No. 0.0037;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLLP 16
 |||||
 Db 13 PLSQETFSGLWKLLP 27

RESULT 11
 JH0631
 cellular tumor antigen p53 - rainbow trout
 C;Species: Oncorhynchus mykiss (rainbow trout)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: JH0631
 R;de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
 Gene 112, 241-245, 1992
 A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
 A;Reference number: JH0631; MUID:92210006; PMID:1339362
 A;Accession: JH0631
 A;Molecule type: mRNA
 A;Residues: 1-396 <DEP>
 A;Experimental source: liver
 A;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactivati
 C;Superfamily: cellular tumor antigen p53
 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
 F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 57.1%; Score 60; DB 1; Length 396;
 Best Local Similarity 76.9%; Pred. No. 0.25;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PLSQETFSDLWKLL 14
 |||||
 Db 11 PLSQESFEDLWKM 23

RESULT 12
 S28857
 Glutamate receptor delta-1 chain precursor - rat
 N;Alternate names: kainate receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
 C;Accession: S28857; S31222
 R;Lomeli, H.; Sprengel, R.; Laurie, D.J.; Koehr, G.; Herb, A.; Seeburg, P.H.; Wisden, W.
 FEBS Lett. 315, 318-322, 1993
 A;Title: The rat delta-1 and delta-2 subunits extend the excitatory amino acid receptor
 A;Reference number: S28857; MUID:93138096; PMID:8422924
 A;Accession: S28857
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-1009 <LOW>
 A;Cross-references: EMBL:Z17238

R.Sprengel, R.
 Submitted to the EMBL Data Library, October 1992
 A:Reference number: S31222
 A:Accession: S31222
 A:Molecule type: mRNA

A:Residues: 83-1009 <SPR>
 A:Cross-references: EMBL:Z12738; NID:G56285; PIDN:CAA78936.1; PID:G56286
 C:Superfamily: glutamate receptor; glutamate receptor homology
 C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-1009/Product: glutamate receptor delta-1 chain #status predicted <MAT>
 F:441-866/Domain: glutamate receptor homology <GRH>
 F:565-584/Domain: transmembrane #status predicted <TM1>
 F:601-621/Domain: transmembrane #status predicted <TM2>
 F:632-654/Domain: transmembrane #status predicted <TM3>
 F:830-851/Domain: transmembrane #status predicted <TM4>
 F:422/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.0%; Score 51.5; DB 2; Length 1009;
 Best Local Similarity 47.4%; Pred. No. 13;
 Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQSTFSDWLKLLPENG 19
 |||: |||: |||: |||:
 Db 698 PLEQDSTFAELWRTISKNG 716

RESULT 13

JH0266
 glutamate receptor delta-1 chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
 C:Accession: JH0266
 R:Yamazaki, M.; Araki, K.; Shibata, A.; Mishina, M.
 Biochem. Biophys. Res. Commun. 183, 886-892, 1992
 A:Title: Molecular cloning of a cDNA encoding a novel member of the mouse glutamate receptor
 A:Reference number: JH0266; MUID:92198486; PMID:1372507
 A:Accession: JH0266
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA

A:Residues: 1-1009 <YAM>
 A:Cross-references: DDBJ:D10171; NID:G220417; PIDN:BA01041.1; PID:G220418
 C:Comment: Glutamate receptor channels mediate most of the fast excitatory synaptic transmission
 C:Superfamily: glutamate receptor; glutamate receptor homology
 C:Keywords: glycoprotein; neurotransmitter receptor; phosphoprotein; transmembrane protein
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-1009/Product: glutamate receptor channel delta-1 chain #status predicted <GLU>
 F:441-866/Domain: glutamate receptor homology <GRH>
 F:565-584/Domain: transmembrane #status predicted <TR1>
 F:603-621/Domain: transmembrane #status predicted <TR2>
 F:632-650/Domain: transmembrane #status predicted <TR3>
 F:831-851/Domain: transmembrane #status predicted <TR4>
 F:131,200,422,498/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:593,713/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 49.0%; Score 51.5; DB 2; Length 1009;
 Best Local Similarity 47.4%; Pred. No. 13;
 Matches 9; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 2 PLSQSTFSDWLKLLPENG 19
 |||: |||: |||: |||:
 Db 698 PLEQDSTFAELWRTISKNG 716

RESULT 14

C64396
 precorrin-2 methyltransferase homolog - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: C64396
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rison, J.D.; Sadow, F.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: C64396
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-230 <BUL>
 A:Cross-references: GB:U67522; GB:L77117; NID:G2826315; PIDN:AAB98764.1; PID:G:592306;
 C:Genetics:
 A:Map position: FOR691742-692434
 A:Start codon: GTG
 C:Superfamily: precorrin-3 methylase

Query Match 47.6%; Score 50; DB 2; Length 230;
 Best Local Similarity 55.6%; Pred. No. 4.5;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 PLSQSTFSDWLKLLPENG 19
 |||: |||: |||: |||:
 Db 101 PTLYSTFSYVWKLKRG 118

RESULT 15

G86715
 racemase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: G86715
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: G86715
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-367 <STO>
 A:Cross-references: GB:AE005176; PID:gl2723640; PIDN:AAK04825.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: yhdB

Query Match 47.6%; Score 50; DB 2; Length 367;
 Best Local Similarity 52.9%; Pred. No. 7.5;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 PLSQSTFSDWLKLLPE 17
 |||: |||: |||: |||:
 Db 54 PFYTSETFADSWKILEE 70

Search completed: February 12, 2003, 10:36:01
 Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:32:56 ; Search time 11 Seconds
(without alignments)
71.641 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWLKLLPENG 19

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	386	1 P53_PIG	Q9tub2 sus scrofa
2	99	94.3	391	1 P53_CAVPO	Q9wur6 cavia porce
3	99	94.3	391	1 P53_RABIT	Q95330 oryctolagus
4	99	94.3	393	1 P53_CERAE	P13481 cercopithec
5	99	94.3	393	1 P53_HUMAN	P04637 homo sapien
6	99	94.3	393	1 P53_MACFA	P56423 macaca fasc
7	99	94.3	393	1 P53_MACMU	P56424 macaca mula
8	99	94.3	393	1 P53_TUPGB	Q9tall tupaia glis
9	94	89.5	382	1 P53_SHEEP	P51664 ovis aries
10	94	89.5	386	1 P53_BOVIN	Q29628 bos taurus
11	94	89.5	391	1 P53_MARMO	Q36006 marmota mon
12	90	85.7	381	1 P53_CANFA	Q29537 canis famil
13	90	85.7	386	1 P53_PELCA	P41685 felis silve
14	86	81.9	393	1 P53_CRIGR	O09185 cricetus
15	86	81.9	396	1 P53_MESAU	Q00366 mesocricetu
16	81	77.1	363	1 P53_XENLA	P07193 xenopus lae
17	74	70.5	390	1 P53_MOUSE	Q02340 mus musculu
18	72	68.6	391	1 P53_RAT	P10361 rattus norv
19	60	57.1	396	1 P53_ONCMY	P25035 oncorhynchu
20	54	51.4	367	1 P53_TETMU	Q96739 tetradodon m
21	53.5	51.0	342	1 P53_XIPHE	O57535 xiphophoru
22	53.5	51.0	342	1 P53_XIPMA	Q92143 xiphophoru
23	50	47.6	230	1 P53_METJA	Q58181 methanococc
24	48	45.7	119	1 IPI_BACSU	P39804 bacillus su
25	48	45.7	1004	1 SLPO_BACBR	P09333 bacillus br
26	47	44.8	156	1 COAT_PMV2	Q9wdg5 pepper mild
27	47	44.8	156	1 COAT_PMV1	Q94843 pepper mild
28	47	44.8	156	1 COAT_PMV5	P29096 pepper mild
29	47	44.8	156	1 COAT_TOMKO	Q83482 tomato mosa
30	47	44.8	158	1 COAT_PMV0	Q9wdg3 pepper mild
31	47	44.8	314	1 P53_SPEBE	Q84662 spermophilu
32	47	44.8	956	1 SYI_AQUAE	O66651 aquifex aeo
33	46	43.8	307	1 YA24_SYNY3	P72926 synechocyst

RESULT 1

ID	P53_PIG	STANDARD;	PRT;	386 AA.
AC	Q9TUB2;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Cellular tumor antigen p53 (Tumor suppressor p53).			
GN	TP53 OR P53.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9623;			
[1]				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99422034; PubMed=10490836;			
RA	Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;			
RT	"Nucleotide sequence of the porcine p53 cDNA, and the detection of			
RT	recombinant porcine p53 expressed in vitro with a variety of anti-p53			
RT	antibodies.";			
RL	Oncogene 18:5005-5009(1999).			
CC	-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces			
CC	growth arrest or apoptosis depending on the physiological			
CC	circumstances and cell type. Involved in cell cycle regulation as			
CC	a trans-activator that acts to negatively regulate cell division			
CC	by controlling a set of genes required for this process. One of			
CC	the activated genes is an inhibitor of cyclin-dependent kinases.			
CC	Apoptosis induction seems to be mediated either by stimulation of			
CC	BAX and FAS antigen expression, or by repression of Bcl-2			
CC	expression.			
CC	-I- SUBUNIT: Binds DNA as a homotrimer (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Nuclear.			
CC	-I- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY			
CC	OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED			
CC	IN MANY TYPES OF CANCER.			
CC	-I- SIMILARITY: BELONGS TO THE P53 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; AF098067; AA04620.1; -.			
CC	HSSP; P04637; 1C26			
CC	InterPro; IPR002117; P53.			
CC	Prfam; PF00870; P53; 1.			
CC	PRINTS; PR00386; P53SUPPRESSR.			
CC	ProDom; PD002681; P53; 2.			
CC	PROSITE; PS00348; P53; 1.			
CC	Anti-oncogene; DNA-binding; Transcription regulation; Activator;			
CC	Nuclear protein; Phosphorylation; Apoptosis.			
CC	DOMAIN 1 45			
CC	DOMAIN BIND 94 285			
CC	BY SIMILARITY.			

P52633 mus musculu
Q13188 homo sapien
P08343 bovine papi
P58879 methanopyru
P05861 simian immu
P31818 simian immu
P11262 simian immu
Q60320 methanococc
P10360 gallus gall
P46207 aquifex pyr
Q00976 kluveromyc
P39847 bacillus su

ALIGNMENTS

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FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 386 AA; 42862 MW; A4C3D8E8DF55162 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 2
P53_CAVPO STANDARD; PRT; 391 AA.
AC Q9WUR6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=99265972; PubMed=10331945;
RA D'Erchia A.M., Pesole G., Tullio A., Saccone C., Sbisa E.;
RT "Guinea pig p53 mRNA: identification of new elements in coding and
RT untranslated regions and their functional and evolutionary
RT implications.";
RL Genomics 58:50-64(1999).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC
CC EMBL; AJ009673; CAB43196.1; -.
CC HSP; P04637; IYCS.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nucleic acid binding; Phosphorylation; Apoptosis.
CC FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 100 290 BY SIMILARITY.
CC FT DOMAIN 323 354 OLIGOMERIZATION.

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FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43287 MW; 321D40702383573E CRC64;

Query Match 94.3%; Score 99; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 3
P53_RABIT STANDARD; PRT; 391 AA.
AC Q95330;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand;
RX MEDLINE=97208869; PubMed=9055811;
RA le Goss F., May P., Ronco P., Caron de Fromental C.;
RT "CDNA cloning and immunological characterization of rabbit p53.";
RL Gene 185:169-173(1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC
CC EMBL; X90592; CAA62216.1; -.
CC HSP; P04637; IYCS.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nucleic acid binding; Phosphorylation; Apoptosis.
CC FT DOMAIN 1 43 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 99 289 BY SIMILARITY.
CC FT DOMAIN 323 354 OLIGOMERIZATION.
CC FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
CC FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).

```


SQ SEQUENCE 391 AA; 43435 MW; 86BD5B8D0B726525 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 391;
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 4

P53 CERAE STANDARD; PRT; 393 AA.

AC P13481;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=90045967; PubMed=2530498;
 RA Rigaudy P., Eckhardt W.;
 RT "Nucleotide sequence of a cDNA encoding the monkey cellular
 phosphoprotein p53.";
 RL Nucleic Acids Res. 17:8375-8375(1989).
 CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression.
 CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 IN MANY TYPES OF CANCER.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 CC -----
 CC EMBL; X16384; CAA34420.1; -.
 CC FIR; S06594; S06594.
 CC HSSP; P04637; IOLG.
 CC InterPro; IPR002117; P53.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC PRODOM; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT BIND 102 292 BY SIMILARITY.
 FT DOMAIN 325 356 OLIGOMERIZATION.
 FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 393 AA; 43696 MW; 9ED285C9A7855D6E CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 5

P53 HUMAN STANDARD; PRT; 393 AA.

AC P04637; Q16848; Q9UBI2;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53) (Phosphoprotein
 p53) (Antigen NY-CO-13).
 GN TP53 OR P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85230577; PubMed=4006916;
 RA Zakut-Houri R., Bienz-Tadmor B., Givol D., Oren M.;
 RT "Human p53 cellular tumor antigen: cDNA sequence and expression in
 COS cells.";
 RL COS cells.";
 RN EMBL J. 4:1251-1255(1985).
 CC [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064416; PubMed=2946935;
 RA Lamb P., Crawford L.;
 RT "Characterization of the human p53 gene.";
 RL Mol. Cell. Biol. 6:1379-1385(1986).
 CC [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85267676; PubMed=3894933;
 RA Harlow E., Williamson N.M., Ralston R., Helfman D.M., Adams T.E.;
 RT "Molecular cloning and in vitro expression of a cDNA clone for human
 cellular tumor antigen p53.";
 RL Mol. Cell. Biol. 5:1601-1610(1985).
 CC [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87083826; PubMed=3025664;
 RA Harris N., Brill E., Shohat O., Prokocimer M., Wolf D., Arai N.,
 RA Rotter V.;
 RT "Molecular basis for heterogeneity of the human p53 protein.";
 RL Mol. Cell. Biol. 6:4650-4656(1986).
 CC [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89108008; PubMed=2905688;
 RA Buchman V.L., Chumakov P.M., Ninkina N.N., Samarina O.P.,
 RA Georgiev G.P.;
 RT "A variation in the structure of the protein-coding region of the
 human p53 gene.";
 RL Gene 70:245-252(1988).
 CC [6]
 RP SEQUENCE OF 101-393 FROM N.A.
 RX MEDLINE=85126934; PubMed=6396087;
 RA Matlashewski G., Lamb P., Pim D., Peacock J., Crawford L.,
 RA Benchimol S.;
 RT "Isolation and characterization of a human p53 cDNA clone: expression
 of the human p53 gene.";
 RL EMBL J. 3:3257-3262(1984).
 CC [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated in Burkitt's lymphoma cell lines.";

EMBO J. 10:2879-2887(1991).
 [8]
 RN SEQUENCE FROM N.A.
 RP Chumakov P.M., Almazov V.P., Jenkins J.R.;
 RA Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
 [9]
 RN SEQUENCE FROM N.A.
 RP Roemuller E.H., Tilanus M.G.J.;
 RA "P53 genomic sequence. Corrections and polymorphism."
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 [10]
 RN SEQUENCE FROM N.A.
 RP Anderson C.W., Kieleczawa J., Allalunis-Turner J.;
 RA "Human p53 from the malignant glioma-derived cell lines M059J and
 RT M059K have a cancer-associated mutation in exon 8."
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 [11]
 RN ALTERNATIVE SPLICING.
 RP MEDLINE=96197761; PubMed=8632903;
 RA Flanagan J.-M., Waridel F., Estreicher A., Vannier A., Limacher J.-M.,
 RA Gilbert D., Iggo K., Frebourg T.;
 RT "The human tumour suppressor gene p53 is alternatively spliced in
 RT normal cells."
 RL Oncogene 12:813-818(1996).
 [12]
 RN NUCLEAR LOCALIZATION SIGNAL.
 RP MEDLINE=90191730; PubMed=2156209;
 RA Addison C., Jenkins J.R., Sturzbecher H.-W.;
 RA "The p53 nuclear localisation signal is structurally linked to a
 RT p34cdc2 kinase motif."
 RL Oncogene 5:423-426(1990).
 [13]
 RN MINIMAL REPRESSION DOMAIN.
 RP PubMed=11007800;
 RA Hong T.M., Chen J.J., Peck K., Yang P.C., Wu C.W.;
 RA "p53 amino acids 339-346 represent the minimal p53 repression
 RT domain."
 RL J. Biol. Chem. 276:1510-1515(2001).
 [14]
 RN PHOSPHORYLATION BY P60/CDC2 AND CYCLIN B/CDC2.
 RP MEDLINE=90280456; PubMed=2141171;
 RA Bischoff J.R., Friedman P.N., Marshak D.R., Prives C., Beach D.;
 RA "Human p53 is phosphorylated by p60-cdc2 and cyclin B-cdc2."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4766-4770(1990).
 [15]
 RN DEPHOSPHORYLATION BY PP2A.
 RP MEDLINE=91172186; PubMed=1848668;
 RA Scheidtmann K.H., Mumby M.C., Rundell K., Walter G.;
 RA "Dephosphorylation of simian virus 40 large-T antigen and p53 protein
 RT by protein phosphatase 2A: inhibition by small-t antigen."
 RL Mol. Cell. Biol. 11:1996-2003(1991).
 [16]
 RN O-GLYCOSYLATION.
 RP MEDLINE=96197773; PubMed=8632915;
 RA Shaw P., Freeman J., Bovey R., Iggo R.;
 RA "Regulation of specific DNA binding by p53: evidence for a role for
 RT O-glycosylation and charged residues at the carboxy-terminus."
 RL Oncogene 12:921-930(1996).
 [17]
 RN STRUCTURE BY NMR OF 319-360.
 RP MEDLINE=94294808; PubMed=8023159;
 RA Clore G.M., Omichinski J.G., Sakaguchi K., Zambano N., Sakamoto H.,
 RA Appella E., Gronenborn A.M.;
 RT "High-resolution structure of the oligomerization domain of p53 by
 RT multidimensional NMR."
 RL Science 265:386-391(1994).
 [18]
 RN STRUCTURE BY NMR OF 325-355.
 RP MEDLINE=95292092; PubMed=7773777;
 RA Lee W., Harvey T.S., Yin Y., Yau P., Litchfield D., Arrowsmith C.H.;
 RA "Solution structure of the tetrameric minimum transforming domain of
 RT p53."
 RL Nat. Struct. Biol. 1:877-890(1994).

[19]
 RN STRUCTURE BY NMR OF 326-354.
 RP MEDLINE=98026899; PubMed=9321402;
 RA McCoy M., Stavridi E.S., Waterman J.L., Wiczorek A.M., Opella S.J.,
 RA Halazonetis T.D.;
 RT "Hydrophobic side-chain size is a determinant of the
 RT three-dimensional structure of the p53 oligomerization domain."
 RL EMBO J. 16:6230-6236(1997).
 [20]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 94-289.
 RP MEDLINE=94294806; PubMed=8023157;
 RA Cho Y., Gorina S., Jeffrey P.D., Pavletich N.P.;
 RA "Crystal structure of a p53 tumor suppressor-DNA complex:
 RT understanding tumorigenic mutations."
 RL Science 265:346-355(1994).
 [21]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 325-356.
 RP MEDLINE=95184011; PubMed=7878469;
 RA Jeffrey P.D., Gorina S., Pavletich N.P.;
 RA "Crystal structure of the tetramerization domain of the p53 tumor
 RT suppressor at 1.7 angstroms."
 RL Science 267:1498-1502(1995).
 [22]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 13-29 IN COMPLEX WITH MDM2.
 RP MEDLINE=97081050; PubMed=8875929;
 RA Kussie P.H., Gorina S., Marechal V., Elenbaas B., Moreau J.,
 RA Levine A.J., Pavletich N.P.;
 RT "Structure of the MDM2 oncoprotein bound to the p53 tumor suppressor
 RT transactivation domain."
 RL Science 274:948-953(1996).
 [23]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 97-287 IN COMPLEX WITH 53BP2.
 RP MEDLINE=97035414; PubMed=8875926;
 RA Gorina S., Pavletich N.P.;
 RT "Structure of the p53 tumor suppressor bound to the ankyrin and SH3
 RT domains of 53BP2."
 RL Science 274:1001-1005(1996).
 [24]
 RN REVIEW.
 RP MEDLINE=94090335; PubMed=8266092;
 RA Harris C.C.;
 RT "p53: at the crossroads of molecular carcinogenesis and risk
 RT assessment."
 RL Science 262:1980-1981(1993).
 [25]
 RN REVIEW ON VARIANTS.
 RP MEDLINE=91289156; PubMed=1905840;
 RA Hoolstein M., Sidransky D., Vogelstein B., Harris C.C.;
 RT "p53 mutations in human cancers."
 RL Science 253:49-53(1991).
 [26]
 RN REVIEW ON VARIANTS.
 RP MEDLINE=96271983; PubMed=8829653;
 RA de Vries E.M.G., Rieck D.O., de Vries T.N., Hartmann A., Blaszyk H.,
 RA Liao D., Soussi T., Kovach J.S., Sommer S.S.;
 RT "Database of mutations in the p53 and APC tumor suppressor genes
 RT designed to facilitate molecular epidemiological analyses."
 RL Hum. Mutat. 7:202-213(1996).
 [27]
 RN VARIANT ARG-72.
 RP MEDLINE=91153807; PubMed=1999338;
 RA Olshwang S., Laurent-Puig P., Vassal A., Salmon R.-J., Thomas G.;
 RT "Characterization of a frequent polymorphism in the coding sequence
 RT of the tp53 gene in colonic cancer patients and a control
 RT population."
 RL Hum. Genet. 86:369-370(1991).
 [28]

Query Match 94.3%; Score 99; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 7.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFDLWKLLEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 6

P53_MACFA
ID - P53 MACFA STANDARD; PRT; 393 AA.

AC P56423;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]

SEQUENCE FROM N.A.

RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; U48957; AAB91535.1; -;
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 102 292 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL.
FT MOD_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43678 MW; EDEEBA1BD3AEAFB8 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;

Best Local Similarity 100.0%; Pred. No. 7.3e-08; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 7

P53 MACMU

ID - P53 MACMU STANDARD; PRT; 393 AA.

AC P56424;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]

SEQUENCE FROM N.A.

RA Khan M.A., Hansen C., Welsh J.A., Bennett W.P.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.

CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L20442; AAA17994.1; -;
DR EMBL; U48956; AAB91534.1; -;
DR HSSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 102 292 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL.
FT MOD_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43655 MW; E212E5E4FE650103 CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;

Best Local Similarity 100.0%; Pred. No. 7.3e-08; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWLKLLPEN 29

RESULT 8

P53_TUPGB
ID P53_TUPGB STANDARD; PRT; 393 AA.
AC Q9TAL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Tupaiia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=93196;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chinensis; TISSUE=Liver;
RA Park U., Lee Y.;
RT "Wild-type p53 sequence of tree shrews.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----
DR EMBL; AF175893; AAF22640.1; -.
DR HSPF; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene, DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 102 292 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 368 387 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 311 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 392 392 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43552 MW; FD9F36603945A1FA CRC64;

Query Match 94.3%; Score 99; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLKLLPEN 18
| | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWLKLLPEN 29

RESULT 9

P53_SHEEP
ID P53_SHEEP STANDARD; PRT; 382 AA.
AC P51664;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95352828; PubMed=7626788;
RA Dequiedt F., Kettmann R., Burny A., Willemis L.;
RT "Nucleotide sequence of the ovine P53 tumor-suppressor cDNA and its genomic organization.";
RL DNA Seq. 5:255-259(1995).

CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----
DR EMBL; X81705; CAA57349.1; -.
DR HSPF; P04637; 1C26.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene, DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 90 281 BY SIMILARITY.
FT DOMAIN 314 345 OLIGOMERIZATION.
FT DOMAIN 357 376 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 300 312 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 381 381 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42809 MW; 4B024076C79C3B2D CRC64;

Query Match 89.5%; Score 94; DB 1; Length 382;
Best Local Similarity 94.4%; Pred. No. 4.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWLKLLPEN 18
| | | | | | | | | | | | | | | | | |
Db 12 PPLSQETFSDLWLKLLPEN 29

RESULT 10
P53_BOVIN

```

ID AC P53_BOVIN STANDARD; PRT; 386 AA.
DT Q29628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
DE TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913, 9915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Liver;
RA MEDLINE=95352829; PubMed=7626789;
RA Dequiedt F., Kettmann R., Burny A., Willems L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
RL DNA Seq. 5:261-264 (1995).
RN [2]
RP SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
RA MEDLINE=96401400; PubMed=8807776;
RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B. indicus; STRAIN=Boran; TISSUE=Blood;
RA Bishop R.P., Gobright E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81704; CAA57348.1; -
DR EMBL; D49825; BAA08629.1; -
DR EMBL; U74486; AAB51214.1; -
DR HSSP; P04637; ITUP.
DR InterPro: IPR002117; P53.
DR PRINTS; PR00870; P53; 1.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;
DR Nuclear protein; Phosphorylation; Apoptosis.
DR DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
DR DOMAIN 1 44 BY SIMILARITY.
DR DNA BIND 94 285 OLIGOMERIZATION.
DR DOMAIN 318 349 BASIC (REPRESSION OF DNA-BINDING).
DR DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
DR DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DR MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT

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FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;

Query Match 89.5%; Score 94; DB 1; Length 386;
Best Local Similarity 94.4%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
   |||||
DB 12 PPLSQETFSDLWNLLPEN 29
   |||||

RESULT 11
P53 MARMO STANDARD; PRT; 391 AA.
AC O3606;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
DE TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97376996; PubMed=9233767;
RA Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT "Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.";
RL Oncogene 15:327-336 (1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001022; CAA04478.1; -
DR HSSP; P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;
DR Nuclear protein; Phosphorylation; Apoptosis.
DR DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
DR DOMAIN 1 44 BY SIMILARITY.
DR DNA BIND 100 290 OLIGOMERIZATION.
DR DOMAIN 323 354 BASIC (REPRESSION OF DNA-BINDING).
DR DOMAIN 366 385 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DR DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DR MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
FT

```

SQ SEQUENCE 391 AA; 43468 MW; E1DE5DB84BA40182 CRC64;

Query Match 89.5%; Score 94; DB 1; Length 391;
Best Local Similarity 94.4%; Pred. No. 4.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
DB 12 PPLSQETFSDLWKLLPEN 29
|||||

RESULT 12
ID P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Velthoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein.";
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watari T., Hasegawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.
RC STRAIN=Beagle;
RX MEDLINE=95323915; PubMed=7600529;
RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RL Cancer Lett. 92:181-186(1995).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and P53 antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC or?send an email to license@isb-sib.ch).
CC
CC EMBL; AF060514; AAC16909.1; -;
CC EMBL; AR020761; BAA78379.1; -;

DR EMBL; S77819; AAB42022.1; -;
DR HSFP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44
FT DOMAIN 89 280
FT DOMAIN 313 344
FT DOMAIN 356 375
FT DOMAIN 299 311
FT MOD_RES 380 380
FT CONFLICT 1 4
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;
Query Match 85.7%; Score 90; DB 1; Length 381;
Best Local Similarity 88.9%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
DB 12 PPLSQETFSDLWKLLPEN 29
|||||

RESULT 13
ID P53_FELCA STANDARD; PRT; 386 AA.
AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TRP53.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
RT hematopoietic tumors.";
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114699; PubMed=8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
RT suppressor gene.";
RL J. Vet. Med. Sci. 55:801-805(1993).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and P53 antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 CC -----
 CC EMBL; D26608; BAA05653.1; -;
 CC EMBL; D16450; BAA03927.1; -;
 CC HSSP; P04637; LOUG.
 CC InterPro; IPR002117; P53.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC ProDom; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 KW DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 94 285
 FT DOMAIN 318 349
 FT DOMAIN 361 380
 FT DOMAIN 304 316
 FT MOD RES 385
 FT CONFLICT 285 285 K -> R (IN REF. 2).
 SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;

Query Match 85.7%; Score 90; DB 1; Length 386;
 Best Local Similarity 88.9%; Pred. No. 1.8e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLSQETFSDLWKLLPEN 18
 DB 12 PLSQETFSDLWKLLPEN 29

RESULT 14

P53 CRIGR STANDARD; PRT; 393 AA.
 AC Q09185; Q64397; P97258; P97788;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chuang W., Mi L.J., Boorstein R.J.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97183659; PubMed=9031625;
 RA Lee H., Larner J.M., Hamlin J.L.;
 RT "Cloning and characterization of Chinese hamster p53 cDNA."
 RL Gene 184:177-183(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic fibroblast;
 RA Shimizu T., Nikaido O., Suzuki F.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.

CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL; Y08900; CAA70108.1; -;
 CC EMBL; Y08901; CAA70109.1; -;
 CC EMBL; U50395; AAC53040.1; -;
 CC EMBL; D86070; BAA13004.1; -;
 CC HSSP; P04637; ITUP.
 CC InterPro; IPR002117; P53.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC ProDom; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 KW DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 102 292
 FT DOMAIN 325 356
 FT DOMAIN 368 387
 FT DOMAIN 311 323
 FT DOMAIN 392 392
 FT MOD_RES 133 133
 FT VARIANT 135 135 C -> W (IN CELL LINE V79-4).
 FT CONFLICT 103 103 Y -> F (IN REF. 2).
 SQ SEQUENCE 393 AA; 43378 MW; 2A7830E788311689 CRC64;
 Query Match 81.9%; Score 86; DB 1; Length 393;
 Best Local Similarity 94.1%; Pred. No. 7.4e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 PLSQETFSDLWKLLPEN 18
 DB 13 PLSQETFSDLWKLLPEN 29
 P53 MESAU
 ID P53 MESAU STANDARD; PRT; 396 AA.
 AC Q00366; P97276;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Syrain; TISSUE=Kidney;
 RX MEDLINE=92210007; PubMed=1555773;
 RA Legros Y., McIntyre P., Soussi T.;
 RT "The cDNA cloning and immunological characterization of hamster p53."
 RL Gene 112:247-250(1992).
 RN [2]
 RP SEQUENCE FROM N.A.

```

RA Hou E.W., Wiseman R.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
DR EMBL; M75144; AAA37085.1; -.
DR EMBL; U07182; AAB41344.1; -.
DR PIR; JH0633; JH0633.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 105 295 BY SIMILARITY.
FT DOMAIN 328 359 OLIGOMERIZATION.
FT DOMAIN 371 390 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 314 326 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 188 188 G -> S (IN REF. 2).
SQ SEQUENCE 396 AA; 43631 MW; 906EF02568099BE3 CRC64;

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Query Match      81.9%; Score 86; DB 1; Length 396;
Best Local Similarity 94.1%; Pred. No. 7.5e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 PLSQETFSDLWKLPPN 18
   |||||
Db 13 PLSQETFSDLWKLPPN 29

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Search completed: February 12, 2003, 10:35:02
Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:33:27 ; Search time 29 Seconds
(without alignments)
134.996 Million cell updates/sec

Title: US-09-403-440A-2

Perfect score: 105

Sequence: 1 PPLSQETFSDLWKLLPENG 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	94.3	32	4	Q9NZD0
2	99	94.3	387	6	Q8SPZ3
3	99	94.3	393	4	Q9UQ61
4	99	94.3	393	4	Q9HAQ8
5	99	94.3	393	4	Q16811
6	99	94.3	393	4	Q16807
7	99	94.3	393	4	Q15086
8	99	94.3	393	4	Q15087
9	99	94.3	393	4	Q15088
10	99	94.3	393	4	Q16808
11	99	94.3	393	4	Q16809
12	99	94.3	393	4	Q16810
13	99	94.3	393	4	Q9BTM4
14	99	94.3	393	4	Q16535
15	94	89.5	387	6	Q9N252
16	88	83.8	390	11	Q920Y0

Q9NP68 homo sapien
Q9ER40 mus musculus
Q70366 mus musculus
Q91XH8 mus musculus
Q9EPP9 rattus norv
Q9EQL0 rattus norv
P89002 praeomys nat
Q9W680 oncorhynch
Q9W681 oncorhynch
Q9W682 oncorhynch
Q92QD2 rhizobium m
Q9NGC8 mya arenari
Q9NGC7 mya arenari
Q9ULK0 homo sapien
Q62640 rattus norv
Q61627 mus musculus
Q9CHK4 lactococcus
Q9XIQ5 arabidopsis
Q8RAS7 thermoplas
Q8T4N3 rhipicephal
Q8YJK2 bruceella me
Q8T7V3 spissula sol
Q9IU98 pepper mild
Q9IU97 pepper mild
Q9IE32 tobacco mos
Q83483 tobacco mos
Q9EJM2 arabidopsis
Q9HUK7 pseudomonas

ALIGNMENTS

RESULT 1

Q9NZD0 ID Q9NZD0 PRELIMINARY; PRT; 32 AA.
AC Q9NZD0;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE P53 tumor suppressor protein (Fragment).
OS TP53.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GLIOMAS AND ASSOCIATED NORMAL TISSUES;
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,
PA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.,
RT "Mutation Detection Utilizing a Novel PCR Approach for Amplification
RT of the p53 Gene from Microdissected Tissue: Application to Archival
RT Tumor Samples.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210309; AAF63442.1;
DR EMBL; AF210308; AAF63442.1; JOINED.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR ProDom; PD002681; P53; 1.
FT NON TER 32
SQ SEQUENCE 32 AA; 3670 MW; F050EA983A90B917 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLPEN 18
Db 12 PPLSQETFSDLWKLLPEN 29

```

RESULT 2
Q8SPZ3 Q8SPZ3 PRELIMINARY; PRT; 387 AA.
AC Q8SPZ3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE P53.
GN P53.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu N., Shiraki T., Yamada T., Nakajima M., Gauthier J.M.,
RA Pfeiffer C.J., Sato S.;
RT "Nucleotide sequence of the p53 cDNA of beluga whale (Delphinapterus
RT leucas).";
RL Gene 0:0-0(2002).
DR EMBL; AF475081; AAL83290.1; -. B4C8BEDBF34A540E CRC64;
SQ SEQUENCE 387 AA; 43033 MW; 43033 MW; 43033 MW;

Query Match 94.3%; Score 99; DB 6; Length 387;
Best Local Similarity 100.0%; Pred. No. 9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
Db 12 PPLSQETFSDLWKLLEN 29

RESULT 3
Q9UQ61 Q9UQ61 PRELIMINARY; PRT; 393 AA.
AC Q9UQ61;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cellular tumor antigen p53.
GN TP53 OR P53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mirzayans R.;
RA Allalunis-Turner M.J., Barron G.M., Day R.S. III, Dobler K.D.,
RX MEDLINE=93303270; PubMed=8316628;
RT "Isolation of two cell lines from a human malignant glioma specimen
RT differing in sensitivity to radiation and chemotherapeutic drugs.";
RL Radiat. Res. 134:349-354(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Anderson C.W., Kiehlczawa J., Allalunis-Turner M.J.;
RT "Human p53 from malignant glioma-derived M059J and M059K cells has a
RT cancer-associated mutation in exon 8.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC RAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF307851; AAG28785.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
KW SEQUENCE 393 AA; 43712 MW; AC611E4938C7BC3B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
Db 12 PPLSQETFSDLWKLLEN 29

RESULT 4
Q9HAQ8 Q9HAQ8 PRELIMINARY; PRT; 393 AA.
AC Q9HAQ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cellular tumor antigen p53.
GN TP53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21264809; PubMed=11058590;
RA Chang N.-S., Pratt N., Heath J., Schultz L., Sleve D., Carey G.B.,
RA Zevotek N.;
RT "Hyaluronidase Induction of a WW Domain-Containing Oxidoreductase that
RT Enhances Tumor Necrosis Factor Cytotoxicity.";
RL J. Biol. Chem. 276:3361-3370(2001).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF307851; AAG28785.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
KW SEQUENCE 393 AA; 43712 MW; AC611E4938C7BC3B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPLSQETFSDLWKLLEN 18
Db 12 PPLSQETFSDLWKLLEN 29

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Qy 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 5

Q16811 ID Q16811 PRELIMINARY; PRT; 393 AA.
 AC Q16811;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cellular tumor antigen p53.
 GN TP53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85126934; PubMed=6396087;
 RA Matlashewski G., Lamb P., Pim D., Peacock J., Crawford L.,
 RA Benchimol S.;
 RT "Isolation and characterization of a human p53 cDNA clone: expression
 of the human p53 gene.";
 RL EMBO J. 3:3257-3262(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064416; PubMed=2946935;
 RA Lamb P., Crawford L.;
 RT "Characterization of the human p53 gene.";
 RL Mol. Cell. Biol. 6:1379-1385(1986).
 CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; M13121; AAA59987.1; JOINED.
 DR EMBL; M13112; AAA59987.1; JOINED.
 DR EMBL; M13113; AAA59987.1; JOINED.
 DR EMBL; M13114; AAA59987.1; JOINED.
 DR EMBL; M13115; AAA59987.1; JOINED.
 DR EMBL; M13116; AAA59987.1; JOINED.
 DR EMBL; M13117; AAA59987.1; JOINED.
 DR EMBL; M13118; AAA59987.1; JOINED.
 DR EMBL; M13119; AAA59987.1; JOINED.
 DR EMBL; M13120; AAA59987.1; JOINED.
 DR HSSP; P04637; ITUP.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 FT NON-TER 193 193
 FT VARIANT 193 193 R -> H.
 FT SEQUENCE 393 AA; 43698 MW; AD1979573AFADA5 CRC64;
 Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

Qy 1 PPLSQETFSDLWKLLPEN 18

Db 12 PPLSQETFSDLWKLLPEN 29
 |||||

RESULT 6

Q16807 ID Q16807 PRELIMINARY; PRT; 393 AA.
 AC Q16807;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cellular tumor antigen p53 (Fragment).
 GN TP53 OR P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
 RL EMBO J. 10:2879-2887(1991).
 CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; X60011; CAA42626.1; -.
 DR HSSP; P04637; IOLG.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 FT NON-TER 193 193
 FT VARIANT 193 193 R -> H.
 FT SEQUENCE 393 AA; 43731 MW; 3A3580718E932E27 CRC64;
 Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 7

Q15086 ID Q15086 PRELIMINARY; PRT; 393 AA.
 AC Q15086;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P53 transformation suppressor (Fragment).
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines.";
 RL EMBO J. 10:2879-2887(1991).
 CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; X60011; CAA42626.1; -.
 DR HSSP; P04637; IOLG.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 FT NON-TER 193 193
 FT VARIANT 193 193 R -> H.
 FT SEQUENCE 393 AA; 43731 MW; 3A3580718E932E27 CRC64;
 Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=92007731; PubMed=1915267;
RA  Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT  "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL  EMBO J. 10:2879-2887(1991).
DR  EMBL; X60013; CAA42628.1; -.
DR  HSSP; P04637; IOLG.
DR  InterPro; IPR002117; P53.
DR  Pfam; PF00870; P53; 1.
DR  PRINTS; PR00386; P53SUPPRESSR.
DR  ProDom; PD002681; P53; 1.
FT  VARIANT 246 246 T -> M.
FT  NON TER 393 393
SQ  SEQUENCE 393 AA; 43662 MW; AC798FCAIEACOBCEB CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PPLSQETPSDLWKLLPEN 18
Db  12 PPLSQETPSDLWKLLPEN 29

RESULT 8
ID Q15087 PRELIMINARY; PRT; 393 AA.
AC Q15087;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P53 transformation suppressor (Fragment).
GN P53.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=92007731; PubMed=1915267;
RA  Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT  "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL  EMBO J. 10:2879-2887(1991).
DR  EMBL; X60014; CAA42629.1; -.
DR  HSSP; P04637; IOLG.
DR  InterPro; IPR002117; P53.
DR  Pfam; PF00870; P53; 1.
DR  PRINTS; PR00386; P53SUPPRESSR.
DR  ProDom; PD002681; P53; 1.
FT  VARIANT 237 237 I -> M.
FT  NON TER 393 393
SQ  SEQUENCE 393 AA; 43694 MW; C6A118E50EB96BB CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PPLSQETPSDLWKLLPEN 18
Db  12 PPLSQETPSDLWKLLPEN 29

RESULT 9
ID Q15088 PRELIMINARY; PRT; 393 AA.
AC Q15088;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P53 transformation suppressor (Fragment).
GN P53.
OS Homo sapiens (Human)

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=92007731; PubMed=1915267;
RA  Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT  "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL  EMBO J. 10:2879-2887(1991).
DR  EMBL; X60016; CAA42631.1; -.
DR  HSSP; P04637; IOLG.
DR  InterPro; IPR002117; P53.
DR  Pfam; PF00870; P53; 1.
DR  PRINTS; PR00386; P53SUPPRESSR.
DR  ProDom; PD002681; P53; 1.
FT  VARIANT 238 238 Y -> C.
FT  NON TER 393 393
SQ  SEQUENCE 393 AA; 43713 MW; AD48ABDB26FA208B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PPLSQETPSDLWKLLPEN 18
Db  12 PPLSQETPSDLWKLLPEN 29

RESULT 10
ID Q16808 PRELIMINARY; PRT; 393 AA.
AC Q16808;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cellular tumor antigen p53 (Fragment).
GN TP53 OR P53.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN  SEQUENCE FROM N.A.
RX  MEDLINE=92007731; PubMed=1915267;
RA  Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
RT  "p53 is frequently mutated Burkitt's lymphoma cell lines.";
RL  EMBO J. 10:2879-2887(1991).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR  EMBL; X60018; CAA42633.1; -.
DR  HSSP; P04637; IOLG.
DR  InterPro; IPR002117; P53.
DR  Pfam; PF00870; P53; 1.
DR  PRINTS; PR00386; P53SUPPRESSR.
DR  ProDom; PD002681; P53; 1.
DR  PROSITE; PS00348; P53; 1.
KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription regulation.
FT  VARIANT 163 163 H -> Y.
FT  NON TER 393 393

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SQ SEQUENCE 393 AA; 43627 MW; 3325FAE63F8E1E61 CRC64;
 Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 11

Q16809 PRELIMINARY; PRT; 393 AA.
 AC Q16809;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cellular tumor antigen p53 (Fragment).
 GN TP53 OR P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines."
 RL EMO J. 10:2879-2887(1991).

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; X60020; CAA42635.1; -;
 DR HSP; P04637; IOLG.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 FT VARIANT 254 254 D -> N.
 FT NON TER 393 393
 FT SEQUENCE 393 AA; 43714 MW; AC69737F2CF9C53B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 13

Q9BTM4 PRELIMINARY; PRT; 393 AA.
 ID Q9BTM4;
 AC Q9BTM4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cellular tumor antigen p53.
 GN TP53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Strausberg R.;
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cellular tumor antigen p53 (Fragment).
 GN TP53 OR P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated Burkitt's lymphoma cell lines."
 RL EMO J. 10:2879-2887(1991).

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; X60020; CAA42635.1; -;
 DR HSP; P04637; IOLG.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 FT VARIANT 254 254 D -> N.
 FT NON TER 393 393
 FT SEQUENCE 393 AA; 43714 MW; AC69737F2CF9C53B CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 DB 12 PPLSQETFSDLWKLLPEN 29

RESULT 13

Q9BTM4 PRELIMINARY; PRT; 393 AA.
 ID Q9BTM4;
 AC Q9BTM4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Cellular tumor antigen p53.
 GN TP53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Strausberg R.;
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-

CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -|- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC EMBL; BC003596; AA03596.1; -.
 CC HSSP; P04637; 10LG.
 CC InterPro; IPR002117; P53.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC PRODOM; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 CC KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 SQ SEQUENCE 393 AA; 43686 MW; 5C701E458E016756 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 14

Q16535 ID Q16535 PRELIMINARY; PRT; 393 AA.
 AC Q16535;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE P53 transformation suppressor (Fragment).
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=92007731; PubMed=1915267;
 RA Farrell P.J., Allan G., Shanahan F., Vousden K.H., Crook T.;
 RT "p53 is frequently mutated in Burkitt's lymphoma cell lines.";
 RL EMO J. 10:2879-2887(1991).
 DR EMBL; X60017; CAA42632.1; -.
 DR EMBL; X60015; CAA42630.1; -.
 DR HSSP; P04637; 10LG.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 FT VARIANT 248 248 Q -> R.
 FT NON TER 393 393
 SQ SEQUENCE 393 AA; 43684 MW; FC5343E85557BC39 CRC64;

Query Match 94.3%; Score 99; DB 4; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

RESULT 15

Q9N252 ID Q9N252 PRELIMINARY; PRT; 387 AA.

AC Q9N252;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 GN Cellular tumor antigen p53.
 DE TP53.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=URINARY BLADDER EPITHELIUM;
 RA Plass M., Hartmann E., Mueller O., Kuhlmann J.;
 RT "Identification of a Sus scrofa gene encoding a protein with high
 RT similarity to p53 from Homo sapiens, Bos taurus and Ovis aries.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -|- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -|- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
 CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
 CC MANY TYPES OF CANCER (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC EMBL; AF124298; AAF28891.1; -.
 CC HSSP; P04637; 1C26.
 CC InterPro; IPR002117; P53.
 CC Pfam; PF00870; P53; 1.
 CC PRINTS; PR00386; P53SUPPRESSR.
 CC PRODOM; PD002681; P53; 1.
 CC PROSITE; PS00348; P53; 1.
 KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription regulation.
 SQ SEQUENCE 387 AA; 43475 MW; 3BB49A432B0053FA CRC64;

Query Match 89.5%; Score 94; DB 6; Length 387;
 Best Local Similarity 94.4%; Pred. No. 5.8e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PPLSQETFSDLWKLLPEN 18
 |||||
 Db 12 PPLSQETFSDLWKLLPEN 29

Search completed: February 12, 2003, 10:35:38
 Job time : 30 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:49:54 ; Search time 15 Seconds
(without alignments)
32.045 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum March 0%

100% Processing: Minimum Match 0%
Maximum Match 100%

Maximum match 100%
Listing first 100 summaries

Database : PIR 73:*

```
1: _pir1:*
```

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2: pir2:*
```

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	11	47.8	5	2	A32516	cholecystokinin-5
2	11	47.8	5	2	A60803	neuropeptide - sea
3	11	47.8	5	2	JH0253	gut pentapeptide -
4	11	47.8	5	2	G37196	bradykinin-potenti
5	11	47.8	5	2	PT0281	Ig heavy chain CRD
6	11	47.8	5	2	PT0308	Ig heavy chain CRD
7	11	47.8	5	2	PT0729	Ig heavy chain CRD
8	11	47.8	5	2	PT0580	T-cell receptor be
9	8	34.8	5	2	PT0278	T-cell receptor be
10	6	26.1	5	2	A44955	Ig heavy chain CRD
11	6	26.1	5	2	S70615	alkanal monooxygen
12	6	26.1	5	2	P00009	endo-1,4-beta-xyla
13	6	26.1	5	2	P50324	angiotensin-conver
14	6	26.1	5	2	B45535	ribulose-bisphosph
15	6	26.1	5	2	A44692	actin I - malaria
16	6	26.1	5	2	B61445	fulicin - giant Af
17	6	26.1	5	2	A61445	Leu-enkephalin - b
18	6	26.1	5	2	J50319	Met-enkephalin - b
19	6	26.1	5	2	B51168	subesophageal gang
20	6	26.1	5	2	PT0644	cocoanase (EC 3.4.
21	6	26.1	5	2	PT0644	T-cell receptor be
22	6	26.1	5	4	A58728	serrawettin W2 - S
23	4	17.4	5	1	H0R0HA	proctolin - Americ
24	4	17.4	5	2	JN0860	peptidyl-dipeptida
25	4	17.4	5	2	C41225	copper resistance
26	4	17.4	5	2	B42364	flagellar protein
27	4	17.4	5	2	B22565	R-phycoerythrin al
28	4	17.4	5	2	S55237	zinc-binding prote
29	4	17.4	5	2	A60411	proctolin - Atlant
30	4	17.4	5	2	S53595	hypothetical prote

ALIGNMENTS

RESULT 1
A32516
cholecystokinin-5 - dog
N;Alternate names: CKK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CKK-5: sequence analysis of a small cholecystokinin from canine brain and intestine
A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
DB 2 W 2

RESULT 2
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60803
R;Graff, D.; Grimmlikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.
A;Reference number: A60803; MUID:88222764; PMID:2897223
A;Accession: A60803
A;Molecule type: protein
A;Residues: 1-5 <GRA>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
DB 5 W 5

RESULT 3
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Usaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
, and of the circular muscle of the gastro-intestinal junction.

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
DB 3 W 3

RESULT 4
G37196
bradykinin-potentiating peptide 7 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: G37196
J;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
R. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
A;Accession: G37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
DB 3 W 3

RESULT 5
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0281
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0281
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
DB 4 W 4

RESULT 6
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0308
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0308
A;Molecule type: DNA

A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
DB 2 W 2

RESULT 7
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0640; PT0685; PT0729
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0640
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A;Accession: PT0685
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A;Accession: PT0729
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE3>
A;Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
DB 5 W 5

RESULT 8
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0580
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0580
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 47.8%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
DB 4 W 4

RESULT 9

PT0278
IG heavy chain CRD3 region (clone 4-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0278
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 34.8%; Score 8; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXL 4
DB 2 FGVL 5

RESULT 10

A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)
C;Species: Vibrio harveyi
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquette, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib

A;Reference number: A44955; MUID:90175700; PMID:2626493
A;Accession: A44955
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 26.1%; Score 6; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 11

S70615
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)
N;Alternate names: xylanase
C;Species: Streptomyces sp.
A;Variety: Chainia sp. NCL 82.5.1
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S70615
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
Biochem. J. 316, 771-775, 1996
A;Title: Structural environment of an essential cysteine residue of xylanase from Chainia

A;Reference number: S70615; MUID:96265041; PMID:8670151
A;Accession: S70615
A;Molecule type: protein
A;Residues: 1-5 <RAO>
A;Experimental source: Chainia sp. strain NCL 82.5.1
A;Note: the source is designated as Chainia sp.
C;Function:

A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
A;Pathway: fermentation of hemicellulose into ethanol
C;Keywords: glycosidase; hydrolase

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
 |
 Db 3 F 3

RESULT 12
 PQ0009
 angiotensin-converting enzyme inhibitor (FLP-2) - common fig
 N;Alternate names: ficus latex peptide 2
 C;Species: Ficus carica (common fig)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
 C;Accession: PQ0009
 R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
 Agric. Biol. Chem. 53, 2763-2767, 1989
 A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
 A;Reference number: PQ0008
 A;Accession: PQ0009
 A;Molecule type: protein
 A;Residues: 1-5 <MAR>
 A;Experimental source: latex
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 |
 Db 1 LY 2

RESULT 13
 PS0324
 ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)
 C;Species: Oryza sativa (rice)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998
 C;Accession: PS0324
 R;Tsugita, A.
 submitted to JIPID, April 1993
 A;Reference number: PS0206
 A;Accession: PS0324
 A;Molecule type: protein
 A;Residues: 1-5 <TSU>
 A;Experimental source: leaf, chlorophyll

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
 |
 Db 1 F 1

RESULT 14
 B45525
 actin I - malaria parasite (Plasmodium falciparum) (fragments)
 C;Species: Plasmodium falciparum
 C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C;Accession: B45525
 R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak
 Mol. Biochem. Parasitol. 35, 167-176, 1989
 A;Title: Stage-specific expression and genomic organization of the actin genes of the ma
 A;Reference number: A45525; MUID:89364996; PMID:2671721
 A;Accession: B45525
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <WES>

A;Cross-references: GB:J03988
 A;Note: the authors translated the codon GAA for residue 3 as Gly
 C;Comment: The actin I gene contains no introns.

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
 |
 Db 5 F 5

RESULT 15
 A44692
 fulicin - giant African snail
 C;Species: Achatina fulica (giant African snail)
 C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
 C;Accession: A44692
 R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No
 Biochem. Biophys. Res. Commun. 178, 486-493, 1991
 A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from t
 A;Reference number: A44692; MUID:91315471; PMID:1859408
 A;Accession: A44692
 A;Molecule type: protein
 A;Residues: 1-5 <OHT>
 C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide
 F;2/Modified site: D-asparagine (Asn) #status experimental
 F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
 |
 Db 1 F 1

RESULT 16
 B61445
 Leu-enkephalin - blue mussel
 C;Species: Mytilus edulis (blue mussel)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
 C;Accession: B61445
 R;Leung, M.K.; Stefano, G.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
 A;Reference number: A61445; MUID:84144823; PMID:6583690
 A;Accession: B61445
 A;Molecule type: protein
 A;Residues: 1-5 <LEU>
 A;Experimental source: pedal ganglia
 C;Keywords: neuropeptide; opioid peptide

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
 |
 Db 4 F 4

RESULT 17
 A61445
 Met-enkephalin - blue mussel
 C;Species: Mytilus edulis (blue mussel)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
 C;Accession: A61445
 R;Leung, M.K.; Stefano, G.B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis

A;Reference number: A61445; MUID:84144823; PMID:6593690
 A;Accession: A61445
 A;Molecule type: protein
 A;Residues: 1-5 <LEU>
 A;Experimental source: pedal ganglia
 C;Keywords: neuropeptide; opioid peptide

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 4 F 4

RESULT 18

JS0319
 subesophageal ganglion pentapeptide - house cricket
 C;Species: Acheta domesticus (house cricket)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C;Accession: JS0319
 R;Wicker, C.; Wicker, C.
 Comp. Biochem. Physiol. C 88, 185-187, 1987
 A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion
 A;Reference number: JS0319
 A;Accession: JS0319
 A;Molecule type: protein
 A;Residues: 1-5 <NIC>

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 5 F 5

RESULT 19

B61168
 cocoanase (EC 3.4.21.-) - Chinese oak silkworm (fragment)
 C;Species: Antheraea pernyi (Chinese oak silkworm)
 C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C;Accession: B61168
 R;Kramer, K.J.; Felsted, R.L.; Law, J.H.
 J. Biol. Chem. 248, 3021-3028, 1973
 A;Title: Cocoanase. V. Structural studies on an insect serine protease.
 A;Reference number: A61168; MUID:73166540; PMID:4735570
 A;Accession: B61168
 A;Molecule type: protein
 A;Residues: 1-5 <KRA>
 C;Keywords: hydrolase; serine proteinase; zymogen
 F;1-5/Product: cocoanase (fragment) #status experimental <MAT>

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 5 F 5

RESULT 20

PT0644
 T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0644
 R;Peeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0644
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 26.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 4 F 4

RESULT 21

A58728
 serrawettin W2 - Serratia marcescens
 C;Species: Serratia marcescens
 C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
 C;Accession: A58728
 R;Matsuyama, I.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and
 A;Reference number: A58728; MUID:92193260; PMID:1548227
 A;Accession: A58728
 A;Status: unencoded polypeptide
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: strain NS 25
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
 C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded
 F;1/Modified site: D-leucine (Leu) #status experimental
 F;4/Modified site: D-phenylalanine (Phe) #status experimental
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match 26.1%; Score 6; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 Db 4 F 4

RESULT 22

H0ROHA
 proctolin - American cockroach
 C;Species: Periplaneta americana (American cockroach)
 C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
 C;Accession: A01644
 R;Starratt, A.N.; Brown, B.E.
 Life Sci. 17, 1253-1256, 1975
 A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects
 A;Reference number: A93048; MUID:76074708; PMID:576
 A;Accession: A01644
 A;Molecule type: protein
 A;Residues: 1-5 <STA>
 A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmac

Science 213, 567-569, 1981
 A;Title: Pentapeptide (proctolin) associated with an identified neuron.
 A;Reference number: A94260; MUID:81225865; PMID:6113690
 A;Contents: annotation; biological source
 C;Comment: This peptide is found in the lateral white neurons, which occur (in the cockr
 innervate the striated hindgut muscles in insects and stimulate contraction of these mus
 C;Superfamily: proctolin
 C;Keywords: neuropeptide

Query Match 17.4%; Score 4; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 3 L 3

RESULT 23
JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0860
R;Watanabe, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
BioSci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
A;Reference number: JN0859; MUID:94080036; PMID:7764272
A;Accession: JN0860
A;Molecule type: protein
A;Residues: 1-5 <MAT>
A;Experimental source: intestine
C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 17.4%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 2 L 2

RESULT 24
C41225
copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: C41225
R;Chen, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: C41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

Query Match 17.4%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 4 L 4

RESULT 25
E42364
flagellar protein fliR - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq
A;Reference number: A42364; MUID:91258342; PMID:1646201
A;Accession: E42364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VOG>
A;Cross-references: GB:M62408

Query Match 17.4%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 4 L 4

RESULT 26
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C;Species: Gastrocloonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 17.4%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 1 L 1

RESULT 27
S55237
zinc-binding protein ZBP14 - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55237
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new family of zin
A;Reference number: S55237; MUID:95234046; PMID:7717986
A;Accession: S55237
A;Molecule type: protein
A;Residues: 1-5 <ROB>

Query Match 17.4%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 1 L 1

RESULT 28
A60411
proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, D.
Peptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab
A;Reference number: A60411; MUID:90287800; PMID:2356151
A;Accession: A60411
A;Molecule type: protein
A;Residues: 1-5 <GRO>
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C;Keywords: neuropeptide

Query Match 17.4%; Score 4; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 3 L 3

RESULT 29

S53595

hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999

C:Accession: S53595

R:Calhoun, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.

Nucleic Acids Res. 22, 5540-5547, 1994

A:Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha

A:Reference number: S53595; MUID:95140613; PMID:7838705

A:Accession: S53595

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <CAL>

A:Cross-references: EMBL:X66844

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 5 L 5

RESULT 30

D44823

synaptosomal-associated protein SNAP-25 peptide 2 - rabbit (fragment)

N:Alternate names: superprotein peptide 2

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996

C:Accession: D44823

R:Loewy, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A:Reference number: A44823; MUID:92044785; PMID:1941090

A:Accession: D44823

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <LOE>

A:Experimental source: visual tissue

A>Note: sequence extracted from NCBI backbone (NCBIP:64250)

C:Keywords: membrane trafficking

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 2 L 2

RESULT 31

PT0624

T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0624

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0624

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 4 L 4

RESULT 32

PT0625

T-cell receptor beta chain V-D-J region (120-2S) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0625

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0625

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 4 L 4

RESULT 33

PT0713

T-cell receptor beta chain V-D-J region (165-3C) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0713

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0713

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
|
Db 4 L 4

RESULT 34

G44817

27.5 kDa structural protein - Leuconostoc oenos phase P32 (fragment)

C:Species: Leuconostoc oenos phase P32

C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

A:Accession: G44817

R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991
 A;Title: Lysogeny in Leuconostoc oenos.
 A;Reference number: A44817; MUID:92085033; PMID:1748868
 A;Accession: G44817
 A;Molecule type: protein
 A;Residues: 1-5 <ARE>
 A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 5 L 5

RESULT 35

I44817
 27.5K structural protein - Leuconostoc oenos phase P37 (fragment)

C;Species: Leuconostoc oenos phase P37
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: I44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: I44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 5 L 5

RESULT 36

E44817
 27.5K structural protein - Leuconostoc oenos phase P54 (fragment)

C;Species: Leuconostoc oenos phase P54
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: E44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: E44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 5 L 5

RESULT 37

C44817
 28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)

C;Species: Leuconostoc oenos phase PAT5-12
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: C44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.
 A;Reference number: A44817; MUID:92085033; PMID:1748868
 A;Accession: C44817
 A;Molecule type: protein
 A;Residues: 1-5 <ARE>
 A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 5 L 5

RESULT 38

A44817

28K structural protein - Leuconostoc oenos phase PZtl1-15 (fragment)

C;Species: Leuconostoc oenos phase PZtl1-15
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: A44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: A44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 5 L 5

RESULT 39

B44817

34.5K structural protein - Leuconostoc oenos phase PZtl1-15 (fragment)

C;Species: Leuconostoc oenos phase PZtl1-15
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: B44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868

A;Accession: B44817

A;Molecule type: protein

A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
 |
 Db 1 L 1

RESULT 40

D44817

35K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)

C;Species: Leuconostoc oenos phase PAT5-12
 C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
 C;Accession: D44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.

J. Gen. Microbiol. 137, 2135-2139, 1991

A;Title: Lysogeny in Leuconostoc oenos.

A;Reference number: A44817; MUID:92085033; PMID:1748868
 A;Accession: D44817
 A;Molecule type: protein
 A;Residues: 1-5 <ARE>
 A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 |
 Db 1 L 1

RESULT 41

S69237
 surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
 C;Species: Staphylothermus marinus
 C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
 C;Accession: S69237
 R;Peters, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
 J. Mol. Biol. 245, 385-401, 1995
 A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua
 A;Reference number: S69237; MUID:95139068; PMID:7837271
 A;Accession: S69237
 A;Molecule type: protein
 A;Residues: 1-5 <PET>
 A;Experimental source: strain F1, DSM 3639
 C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 17.4%; Score 4; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 |
 Db 3 L 3

RESULT 42

JT0870
 phytoulfokine alpha - garden asparagus (fragment)
 C;Species: Asparagus officinalis (garden asparagus)
 C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 19-Apr-2002
 C;Accession: JT0870
 R;Matsubayashi, Y.; Sakagami, Y.
 Proc. Natl. Acad. Sci. U.S.A. 93, 7623-7627, 1996
 A;Title: Phytoulfokine, sulfated peptides that induce the proliferation of single mesoph
 A;Reference number: JT0870
 A;Accession: JT0870
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>

Query Match 17.4%; Score 4; DB 3; Length 5;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 |
 Db 2 IV 3

RESULT 43

B37325
 pap fibrial regulatory protein papI - Escherichia coli (fragment)
 C;Species: Escherichia coli
 C;Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
 C;Accession: B37325
 R;Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
 J. Bacteriol. 173, 1789-1800, 1991
 A;Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
 A;Reference number: A37325; MUID:91154136; PMID:1671857

A;Accession: B37325
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5 <BRA>
 A;Cross-references: GB:M63747

Query Match 13.0%; Score 3; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 4 Y 4

RESULT 44

I39964
 ribosomal protein S4 - Bacillus circulans (fragment)
 C;Species: Bacillus circulans
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
 C;Accession: I39964
 R;Grundy, F.J.; Henkin, T.M.
 J. Bacteriol. 174, 6763-6770, 1992
 A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
 A;Reference number: I39963; MUID:93015735; PMID:1400226
 A;Accession: I39964
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-5 <RES>
 A;Cross-references: GB:M99041; NID:g143471
 C;Genetics:
 A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 4 Y 4

RESULT 45

I39966
 ribosomal protein S4 - Bacillus licheniformis (fragment)
 C;Species: Bacillus licheniformis
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
 C;Accession: I39966
 R;Grundy, F.J.; Henkin, T.M.
 J. Bacteriol. 174, 6763-6770, 1992
 A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
 A;Reference number: I39963; MUID:93015735; PMID:1400226
 A;Accession: I39966
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-5 <RES>
 A;Cross-references: GB:M99043; NID:g143475
 C;Genetics:
 A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 2.8e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 |
 Db 4 Y 4

RESULT 46

I39965
 ribosomal protein S4 - Bacillus megaterium (fragment)
 C;Species: Bacillus megaterium

C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C;Accession: I39965

J;Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A;Title: Characterization of the *Bacillus subtilis* rpsD regulatory target site.

A;Reference number: I39963; MUID:93015735; PMID:1400226

A;Accession: I39965

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: GB:M99042; NID:gl43473

C;Genetics:

A;Gene: rpsD

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 4 Y 4

RESULT 47

I40469

dnazX-like protein - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000

C;Accession: I40469

R;Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A;Title: Transcription and processing of *Bacillus subtilis* small cytoplasmic RNA.

A;Reference number: I40469; MUID:89218958; PMID:2468993

A;Accession: I40469

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-5 <RES>

A;Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204

C;Genetics:

A;Start codon: GTG

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 3 Y 3

RESULT 48

E60274

major protein antigen MPT63 - *Mycobacterium tuberculosis* (fragment)

C;Species: *Mycobacterium tuberculosis*

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: E60274

R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture

A;Reference number: A60274; MUID:9109989; PMID:1898899

A;Accession: E60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 2 Y 2

RESULT 49

F22565

R-phycoerythrin gamma-A chain - red alga (*Gastrocloonium coulteri*) (fragment)

C;Species: *Gastrocloonium coulteri*

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C;Accession: F22565

J;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: F22565

A;Molecule type: protein

A;Residues: 1-5 <KLO>

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 4 Y 4

RESULT 50

PQ0689

Photosystem I 10.4K H1 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0689

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psal, psaE, psaF, psaH and psal are a

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0689

A;Molecule type: protein

A;Residues: 1-5 <OBO>

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 2 Y 2

RESULT 51

S68326

blood cell protein B - *Ascidia ceratodes* (fragment)

N;Alternate names: Abcp-B

C;Species: *Ascidia ceratodes*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999

C;Accession: S68326

R;Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A;Reference number: S68325; MUID:96132650; PMID:8554314

A;Accession: S68326

A;Molecule type: protein

A;Residues: 1-5 <TAY>

F;2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

F;4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 13.0%; Score 3; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
: :
Db 2 Y 2

RESULT 52

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A:Reference number: A60521; MUID:90227907; PMID:2103669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Superfamily: phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

;

Db 2 I 2

RESULT 53

JN0862
peptidyl-dipeptidase A inhibitory peptide C112 - striped bonito
C:Species: Sarda orientalis (striped bonito)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: JN0862
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide
A:Reference number: JN0859; MUID:94080036; PMID:7764272
A:Accession: JN0862
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: intestine
A:Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

;

Db 1 I 1

RESULT 54

B41225
copper resistance protein B - Pseudomonas syringae pv. tomato (fragment)
C:Species: Pseudomonas syringae pv. tomato
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C:Accession: B41225
R:Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane proteins
A:Reference number: A41225; MUID:92020961; PMID:1924351
A:Accession: B41225
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CHA>

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

;

Db 5 M 5

RESULT 55

S70154
URF2 protein - Xanthomonas sp.
C:Species: Xanthomonas sp.
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S70154
R:Khododil, G.Y.; Mindlin, S.Z.; Baes, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforov, M.I. Microbiol. 17, 1189-1200, 1995
A:Title: Four genes, two ends, and a res region are involved in transposition of Tn5053
A:Reference number: S70140; MUID:96130850; PMID:8594337
A:Accession: S70154
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <KHO>
A:Cross-references: EMBL:L40585; NID:G710572; PIDN:AAA98329.1; PID:G735909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

;

Db 1 M 1

RESULT 56

I40702
primase - Citrobacter diversus (fragment)
C:Species: Citrobacter diversus
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
C:Accession: I40702
R:Versalovic, J.; Lupski, J.R.
Mol. Microbiol. 8, 343-355, 1993
A:Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS) genes
A:Reference number: I40702; MUID:93302510; PMID:8316085
A:Accession: I40702
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:L01754; NID:G144439
C:Genetics:
A:Gene: dnaG

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

;

Db 1 M 1

RESULT 57

I40698
biotin B - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: I40698
R:Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: I40697; MUID:89006280; PMID:2971595
A:Accession: I40698
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A;Cross-references: GB:M21922; NID:gl44434

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 1 M 1
Db

RESULT 58

B31836
20K protein - Rickettsia rickettsii (fragment)
C;Species: Rickettsia rickettsii
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C;Accession: B31836
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii
A;Reference number: A91885; MUID:8908059; PMID:3139629
A;Accession: B31836
A;Molecule type: DNA
A;Residues: 1-5 <AND>
A;Cross-references: GB:J03371; NID:gl52455; PIDN:AAI15030.1; PID:g4262874

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 1 M 1
Db

RESULT 59

T10954
hypothetical protein 3 - spring vetch
C;Species: Vicia sativa (spring vetch, tare)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T10954
R;Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.C.; Bisse
submitted to the EMBL Data Library, December 1995
A;Description: A novel type of DNA binding protein interacts with a conserved sequence in
A;Reference number: Z17228
A;Accession: T10954
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5 <CHR>
A;Cross-references: EMBL:X95995; NID:gl360633; PID:e225862

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 1 M 1
Db

RESULT 60

T14908
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14908
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-5 <KIR>

A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 1 M 1
Db

RESULT 61

T14910
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14910
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14910
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905
A;Experimental source: ssp. Hamburger Schnitt

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 1 M 1
Db

RESULT 62

B37988
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
C;Species: Physarum polycephalum
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
C;Accession: B37988
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og
J. Biol. Chem. 265, 19898-19903, 1990
A;Title: Purification and characterization of a novel intracellular acid proteinase from
A;Reference number: A37988; MUID:91060608; PMID:2246266
A;Accession: B37988
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MUR>

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
: 5 I 5
Db

RESULT 63

A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragm
C;Species: Schistosoma mansoni
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C;Accession: A37114
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Fur
A;Reference number: A37114; MUID:90337955; PMID:2199439

A:Accession: A37114
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <YUA>
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 1 M 1

RESULT 64

I50385

myosin light chain 2 - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997

C:Accession: I50385

R:Shen, R.; Goswami, S.K.; Mascareno, E.; Kumar, A.; Siddiqui, M.A.Q.

Mol. Cell. Biol. 11, 1676-1685, 1991

A:Title: Tissue-specific transcription of the cardiac myosin light-chain 2 gene is regul

A:Reference number: I50385; PMID:1996116

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <SHE>

A:Cross-references: GB:M63969; NID:G212332

C:Genetics:

A:Gene: MLC2

Query Match

Best Local Similarity 8.7%; Score 2; DB 2; Length 5;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 1 M 1

RESULT 65

S62883

seminal plasma protein II - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C:Accession: S62883

R:Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.

FEBS Lett. 382, 15-17, 1996

A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal plas

A:Reference number: S62883; PMID:8612739

A:Accession: S62883

A:Molecule type: protein

A:Residues: 1-5 <ROM>

A:Complex: heterodimer; seminal plasma protein I and seminal plasma protein II

C:Keywords: glycoprotein; heterodimer; semen

Query Match

Best Local Similarity 8.7%; Score 2; DB 2; Length 5;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 3 I 3

RESULT 66

B44823

synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)

N:Alternate names: superprotein peptide 10A

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996

C:Accession: B44823

R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A:Reference number: A44823; PMID:92044785; PMID:1941090

A:Accession: B44823

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <LOE>

A:Experimental source: visual tissue

A:Note: sequence extracted from NCBI backbone (NCBIP:64255)

C:Keywords: membrane trafficking

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 3 M 3

RESULT 67

PT0597

T-cell receptor beta chain V-D-J region (111-1B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0597

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0597

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 4 I 4

RESULT 68

PT0590

T-cell receptor beta chain V-D-J region (141-1B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0590

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0590

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
; :
Db 3 M 3

RESULT 69

P0572
T-cell receptor beta chain V-D-J region (141-100) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: P0572
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: P0509; MUID:91277601; PMID:1711558
A:Accession: P0572
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 4 I 4

RESULT 70

H44817
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C:Species: Leuconostoc oenos phase P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 1 M 1

RESULT 71

F44817
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C:Species: Leuconostoc oenos phase P54
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 1 M 1

RESULT 72

S11127
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C:Accession: S11127; S11128
R:Mikuni-Takagaki, Y.; Glincher, M.J.
Biochem. J. 288, 585-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification
A:Reference number: S11127; MUID:90303246; PMID:2363696
A:Accession: S11127
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MIKI>
A:Accession: S11128
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 2-5 <MIK2>
C:Keywords: phosphoprotein

Query Match 4.3%; Score 1; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 L 4
Db 3 V 3

RESULT 73

C23751
spinal cord peptide SCP-6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C:Accession: C23751
R:Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: C23751
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <HSI>
C:Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2
Db 2 A 2

RESULT 74

A26830
mitosis inhibiting peptide - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: A26830
R:Reichelt, K.; Elgjo, K.; Edminson, P.D.
Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
A:Reference number: A26830; MUID:87298602; PMID:3619940
A:Accession: A26830
A:Molecule type: protein
A:Residues: 1-5 <REI>
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; pyroglutamic acid
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2

Db 4 S 4

RESULT 75

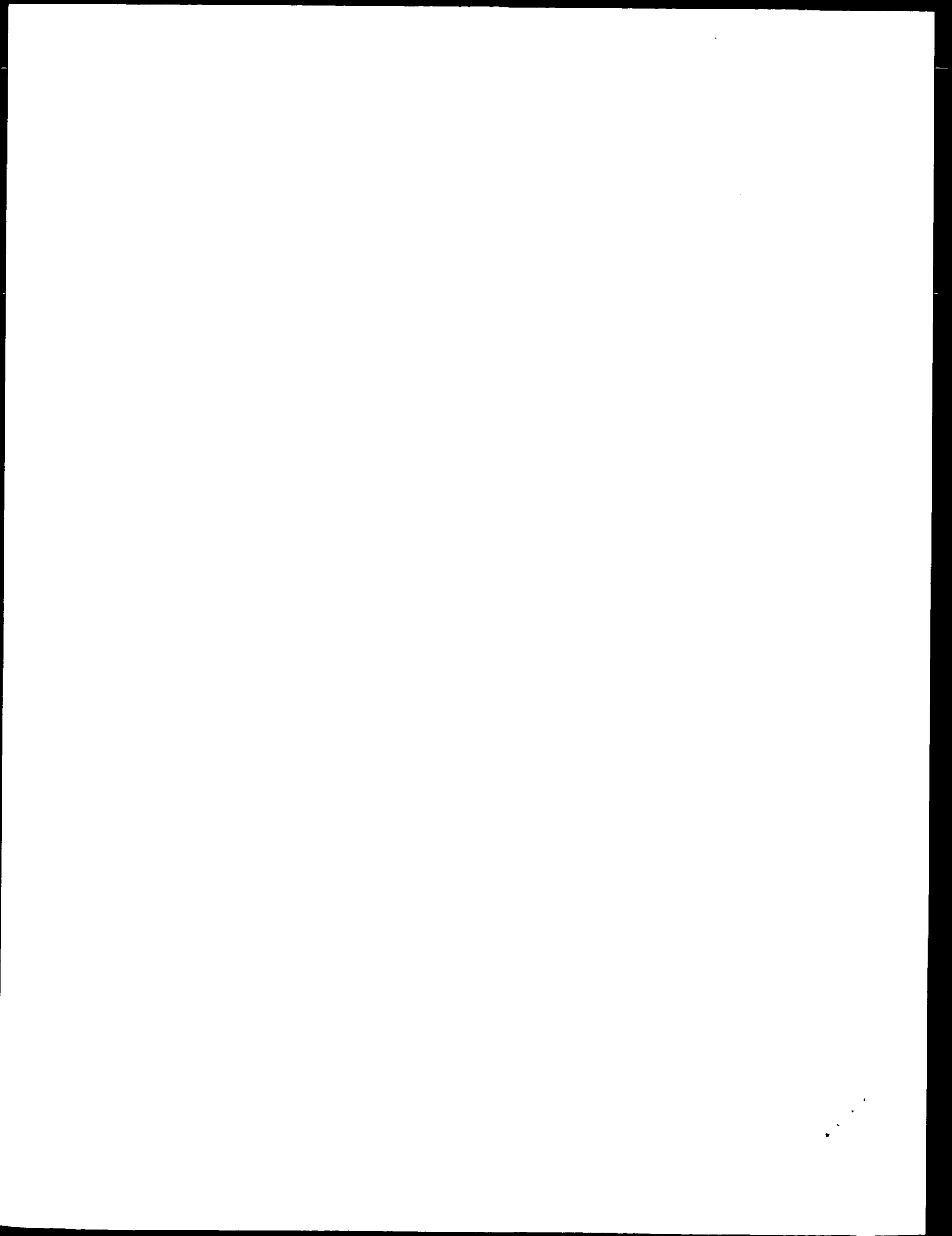
A41225
copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: A41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: A41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

Query Match 0.0%; Score 0; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 2.8e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 X 2

Db 1 A 1

Search completed: February 12, 2003, 10:52:50
Job time : 17 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:46:33 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-403-440A-1
Perfect score: 23
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11	47.8	5	1 BPP7 BOTIN	P30425 bothrops in
2	11	47.8	5	1 UF01 MOUSE	P38639 mus musculu
3	6	26.1	5	1 AL14 CARMA	P81817 carcinus ma
4	6	26.1	5	1 E103 LITRU	P82099 litoria rub
5	6	26.1	5	1 E104 LITRU	P82100 litoria rub
6	6	26.1	5	1 FARP ARTTR	P41853 artiopeathi
7	6	26.1	5	1 PAP2 PARMA	P81864 pardachirus
8	6	26.1	5	1 RE11 LITRU	P82070 litoria rub
9	6	26.1	5	1 RE21 LITRU	P82071 litoria rub
10	6	26.1	5	1 RE31 LITRU	P82072 litoria rub
11	6	26.1	5	1 RE32 LITRU	P82073 litoria rub
12	6	26.1	5	1 SUGA ACHDO	P19991 acheta dome
13	6	26.1	5	1 TPIS CANPA	P54714 canis fami
14	6	26.1	5	1 UC22 MAIZE	P80628 zea mays (m
15	4	17.4	5	1 PRCT PERAM	P01373 periplaneta
16	4	17.4	5	1 PSK DAUCA	P58261 daucus caro
17	2	8.7	5	1 BIOA CITFR	P13071 citrobacter
18	2	8.7	5	1 BIOB CITFR	P12997 citrobacter
19	0	0.0	5	1 TRM3 ECOLI	P13973 escherichia
20	0	0.0	5	1 UXA4 CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1
BPP7 BOTIN
ID BPP7 BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide 85,2 (5A) (Angiotensin-converting

DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

RESULT 2

UF01 MOUSE
ID UF01 MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP NCBI_TaxID=10090;
RC SEQUENCE
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 KDa.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 47.8%; Score 11; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 1 W 1

RESULT 3

AL14 CARMA
ID AL14 CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 5 5
 FT AMIDATION (POTENTIAL).
 SQ SEQUENCE 5 AA; 586 MW; 672879DSAB300000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

Qy 1 F 1
 |
 Db 3 F 3

RESULT 4
 E103_LITRU
 ID E103_LITRU STANDARD; PRT; 5 AA.
 AC P82039;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electrin 3
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5
 FT AMIDATION.
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

Qy 1 F 1
 |
 Db 1 F 1

RESULT 5
 E104_LITRU
 ID E104_LITRU STANDARD; PRT; 5 AA.
 AC P82100;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Electrin 4.

OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5
 FT AMIDATION.
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

Qy 1 F 1
 |
 Db 1 F 1

RESULT 6
 FARP_ARTTR
 ID FARP_ARTTR STANDARD; PRT; 5 AA.
 AC P41853;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide RYIRF-amide.
 OS Actinopterygii; Teleostei; Teleostei; Euteleostei; Neoteleostei;
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Terricola; Geoplanidae; Arthurdendyus.
 OX NCBI_TaxID=132421;
 [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94211927; PubMed=7909164;
 RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "RYIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
 RL Regul. Pept. 50:37-43(1994).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 5 5
 FT AMIDATION.
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B46000000 CRC64;

Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0;

Qy 1 F 1
 |
 Db 5 F 5

RESULT 7
 PAP2_PARMA
 ID PAP2_PARMA STANDARD; PRT; 5 AA.
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pardaxin II (PXII) (Fragment).
 OS Pardachirus marmoratus (Red sea moles sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Soleioidae; Soleidae; Pardachirus.

OX NCBI_TaxID=31087;
 RP [1]
 RN SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=87057369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 RT "Purification from pore-forming activity of two hydrophobic
 RT polypeptides from the secretion of the Red sea moses sole (Pardachirus
 RT marmoratus).";
 RL J. Biol. Chem. 261:16704-16713(1986).
 CC -!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
 CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
 CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
 CC -!- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
 KW Toxin.
 FT NON TER
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 F 1
 DB 2 F 2

 RESULT 8
 RE11_LITRU
 ID RE11_LITRU STANDARD; PRT; 5 AA.
 AC P82070;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9C82A000000 CRC64;

 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 F 1
 DB 3 F 3

 RESULT 9
 RE21_LITRU
 ID RE21_LITRU STANDARD; PRT; 5 AA.
 AC P82071;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 2.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 626 MW; 6DD9C9C810300000 CRC64;

 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 F 1
 DB 3 F 3

 RESULT 10
 RE31_LITRU
 ID RE31_LITRU STANDARD; PRT; 5 AA.
 AC P82072;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9C810300000 CRC64;

 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 F 1
 DB 3 F 3

 RESULT 11
 RE32_LITRU

ID RE32 LITRU STANDARD; PRT; 5 AA.
 AC P82073;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 Litoria electrica. Comparison with the skin peptides from Litoria
 rubella.";
 RL Aust. J. Chem. 52:639-645(1999).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 CC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.
 KM
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 DB 3 F 3

RESULT 12
 SUGA_ACHDO STANDARD; PRT; 5 AA.
 AC P19931;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Subesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
 OC Gryllidae; Gryllinae; Acheta.
 OX NCBI_TaxID=6997;
 RN [1]
 RP SEQUENCE.
 RA Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 subesophageal ganglion of Acheta domesticus (orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
 CC GANGLIA.
 DR PIR; JS0319.
 SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 DB 5 F 5

RESULT 13
 TPIS_CANFA STANDARD; PRT; 5 AA.
 ID TPIS_CANFA
 AC P54714;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
 GN TP11.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-
 CC phosphate.
 CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR HSC-2DPAGE; P54714; DOG.
 DR InterPro; IPR000652; Triophos_ismrse.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON_TER 1 1
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 DB 1 F 1

RESULT 14
 UC22_MAIZE STANDARD; PRT; 5 AA.
 ID UC22_MAIZE
 AC P80628;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
 DR Maize-2DPAGE; P80628; COLEOPTILE.
 DR MaizeDB; 123954; -.
 FT NON_TER 1 1
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;
 Query Match 26.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
 DB 1 F 1

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Db      4 |
        2 F 2

RESULT 15
PCT_PERAM
ID_PCT_PERAM STANDARD; PRT; 5 AA.
AC F01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattoidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Bircksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
DB 3 L 3

RESULT 16
PSK_DAUCA
ID_PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. US-Harumakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kanada H., Sakagami Y.;
RT "A separated peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC -!- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-BETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA; 687 MW; 76C1BB504B300000 CRC64;

Query Match 17.4%; Score 4; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 2 IY 3

RESULT 17
BIOA_CITFR
ID_BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.

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CC -----
 CC EMBL; M21922; ; NOT ANNOTATED CDS.
 CC InterPro; IPR000954; AminoTran_3.
 CC PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
 CC Biotin biosynthesis; Transferase; AminoTransferase;
 CC Pyridoxal phosphate. 5
 CC NON_TER 5
 CC SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; 0; Indels 0; Gaps 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 Db 1 M 1

RESULT 18

ID BIOT_CITFR STANDARD; PRT; 5 AA.
 AC P12997;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment).
 GN BIOT.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89006280; PubMed=2971595;
 RA Shivan D., Campbell A.;
 RT "Transcriptional regulation and gene arrangement of Escherichia coli,
 RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
 RL Gene 67:203-211(1988).
 CC -|- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
 CC -|- PATHWAY: Biotin biosynthesis; last step.
 CC -|- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
 CC FAMILY.

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CC EMBL; M21922; ; NOT ANNOTATED CDS.
 CC Biotin biosynthesis; Iron-sulfur; Transferase.
 CC NON_TER 5
 CC SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 8.7%; Score 2; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; 0; Indels 0; Gaps 0;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 Db 1 M 1

RESULT 19

Query Match 0.0%; Score 0; DB 1; Length 5;

TRM3_ECOLI STANDARD; PRT; 5 AA.
 ID TRM3_ECOLI
 AC P13973;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TrmM protein (Fragment).
 GN TRAM.

OS Escherichia coli.
 OG Plasmid IncFII R100.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88227859; PubMed=2836369;
 RA Inamoto S., Yoshioka Y., Ohtsubo E.;
 RT "Identification and characterization of the products from the traJ
 RT and traY genes of plasmid R100.";
 RL J. Bacteriol. 170:2749-2757(1988).
 CC -|- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
 CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -|- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.

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CC EMBL; M20941; ; NOT ANNOTATED CDS.
 CC PIR; A32014; A32014.
 CC Conjugation; Plasmid; DNA-binding.
 CC NON_TER 1
 CC SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1.1e+05; 1; Indels 0; Gaps 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 X 2
 Db 1 K 1

RESULT 20

ID UXAA4_CHLTR STANDARD; PRT; 5 AA.
 AC P38005;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE.

PC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christianen G., Birkelund S., Viretten E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.5, ITS MW IS: 28 kDa.
 CC Sienra-2DPAGE; P38005; -.
 CC NON_TER 5
 CC SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

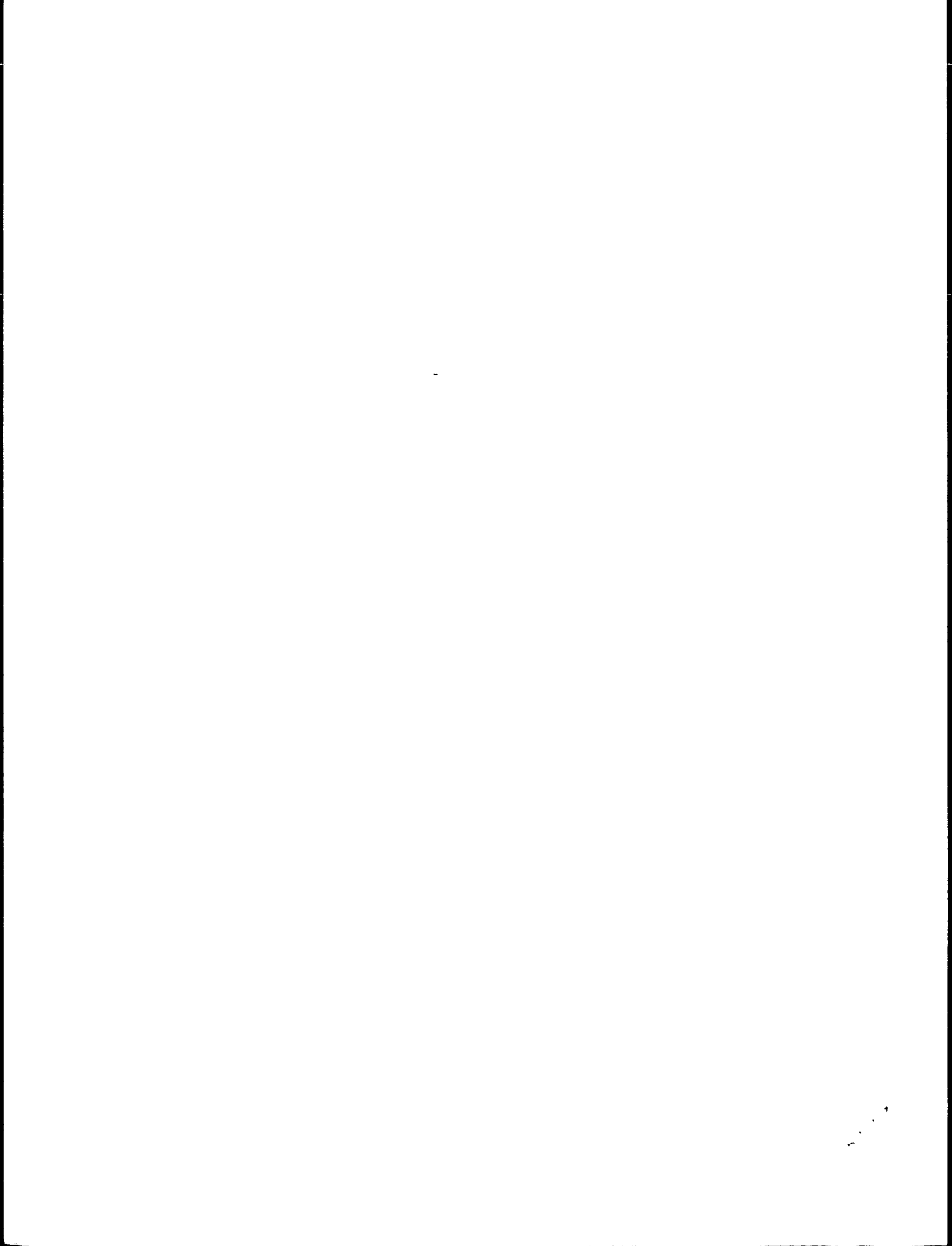
Query Match 0.0%; Score 0; DB 1; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.1e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 X 2

Db 2 S 2

Search completed: February 12, 2003, 10:51:53
Job time : 12 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:48:54 ; Search time 28 Seconds
(without alignments)

36.794 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organalle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	26.1	5	13 P83308	P83308 gallus gall
2	2	8.7	5	2 P83073	P83073 bacillus ce
3	2	8.7	5	10 Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=BRAIN;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide.";
RL Nature 305:328-330(1993).
CC -|- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 26.1%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

DB 5 F 5

RESULT 2

ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 11796;
RA Browne N., Dows B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 8.7%; Score 2; DB 2; Length 5;
Best Local Similarity 0.0%; Pred. No. 6.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4

DB 1 M 1

RESULT 3

ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721 (1991).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR ENBL; X54643; CAA38455.1; --
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON TER 5 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 8.7%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 L 4
 Db 1 M 1

Search completed: February 12, 2003, 10:52:27
 Job time : 28 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:45:58 ; Search time 80 Seconds
(without alignments)
8.328 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXKLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 13629

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq 101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	87.0	5	20	AA193038
2	20	87.0	5	21	AA193038
3	19	82.6	5	17	AA17808
4	19	82.6	5	17	AA189911
5	19	82.6	5	17	AA189912
6	19	82.6	5	21	AA1958280
7	19	82.6	5	23	AA1958280
8	17	73.9	5	13	AA1929438
9	17	73.9	5	13	AA1929438
10	17	73.9	5	15	AA1929438

11	73.9	5	15	AA1929438	Endothelin C-termi
12	73.9	5	15	AA1929438	Endothelin C-termi
13	65.2	5	12	AA193339	Endothelin antag
14	65.2	5	12	AA193339	Endothelin antag
15	65.2	5	12	AA193339	Endothelin antag
16	65.2	5	12	AA193339	Endothelin antag
17	65.2	5	14	AA1938437	Endothelin recepto
18	65.2	5	14	AA1938437	Endothelin recepto
19	65.2	5	14	AA1938437	Endothelin recepto
20	65.2	5	14	AA1938437	Endothelin recepto
21	65.2	5	14	AA1938437	Endothelin recepto
22	65.2	5	14	AA1938437	Endothelin recepto
23	65.2	5	14	AA1938437	Endothelin recepto
24	65.2	5	14	AA1938437	Endothelin recepto
25	65.2	5	14	AA1938437	Endothelin recepto
26	65.2	5	14	AA1938437	Endothelin recepto
27	65.2	5	14	AA1938437	Endothelin recepto
28	65.2	5	14	AA1938437	Endothelin recepto
29	65.2	5	15	AA1938437	Endothelin metal c
30	65.2	5	15	AA1938437	Cyclic peptide whi
31	65.2	5	15	AA1938437	Monomeric peptide
32	65.2	5	15	AA1938437	TAN-1462A - cyclic
33	65.2	5	15	AA1938437	TAN-1462B - cyclic
34	65.2	5	15	AA1938437	TAN-1477K - cyclic
35	65.2	5	15	AA1938437	CENP-B protein res
36	65.2	5	15	AA1938437	Endothelin cyclic
37	65.2	5	15	AA1938437	Cyclic pentapeptid
38	65.2	5	15	AA1938437	Cyclic pentapeptid
39	65.2	5	15	AA1938437	Cyclic pentapeptid
40	65.2	5	15	AA1938437	Cyclic pentapeptid
41	65.2	5	15	AA1938437	Cyclic pentapeptid
42	65.2	5	15	AA1938437	Cyclic pentapeptid
43	65.2	5	15	AA1938437	Endothelin cyclic
44	65.2	5	15	AA1938437	Endothelin cyclic
45	65.2	5	15	AA1938437	Endothelin cyclic
46	65.2	5	16	AA1938437	DP-118 homologue 3
47	65.2	5	16	AA1938437	Melanin pigmentati
48	65.2	5	16	AA1938437	Melanin pigmentati
49	65.2	5	16	AA1938437	Melanin pigmentati
50	65.2	5	16	AA1938437	Cyclic endothelin
51	65.2	5	16	AA1938437	Cyclic endothelin
52	65.2	5	16	AA1938437	Cyclic endothelin
53	65.2	5	16	AA1938437	Cyclic endothelin
54	65.2	5	16	AA1938437	Endothelin antag
55	65.2	5	16	AA1938437	Endothelin antag
56	65.2	5	17	AA1938437	Cyclic pentapeptid
57	65.2	5	17	AA1938437	Targetting conjuga
58	65.2	5	18	AA1938437	Targetting conjuga
59	65.2	5	18	AA1938437	Targetting conjuga
60	65.2	5	18	AA1938437	Targetting conjuga
61	65.2	5	18	AA1938437	Targetting conjuga
62	65.2	5	18	AA1938437	Targetting conjuga
63	65.2	5	18	AA1938437	Conjugating cyclic
64	65.2	5	18	AA1938437	Low density lipopr
65	65.2	5	18	AA1938437	Low density lipopr
66	65.2	5	18	AA1938437	Low density lipopr
67	65.2	5	19	AA1938437	Human microtubule
68	65.2	5	19	AA1938437	Endothelin recepto
69	65.2	5	19	AA1938437	Cyclic peptide whi
70	65.2	5	19	AA1938437	Cyclic peptide whi
71	65.2	5	20	AA1938437	Non-crosslinked pr
72	65.2	5	20	AA1938437	Acetyl choline (mu
73	65.2	5	20	AA1938437	Antigenic peptide
74	65.2	5	20	AA1938437	Fibrinogen peptide
75	65.2	5	21	AA1938437	T20/DP178 peptide
76	65.2	5	21	AA1938437	T20/DP178 peptide
77	65.2	5	21	AA1938437	Protein encoded by
78	65.2	5	21	AA1938437	HIV-1 isolate LAI
79	65.2	5	21	AA1938437	EGIII-like cellula
80	65.2	5	21	AA1938437	Endothelin recepto
81	65.2	5	21	AA1938437	Endothelin recepto
82	65.2	5	21	AA1938437	Endothelin recepto
83	65.2	5	21	AA1938437	Hepatitis GB virus

84 15 65.2 5 21 AAY97920 Endothelin recepto
 85 15 65.2 5 21 AAY97921 Endothelin recepto
 86 15 65.2 5 21 AAY97922 Endothelin recepto
 87 15 65.2 5 21 AAY97935 Endothelin recepto
 88 15 65.2 5 21 AAY97936 Endothelin recepto
 89 15 65.2 5 21 AAY97937 Endothelin recepto
 90 15 65.2 5 21 AAY97950 Endothelin recepto
 91 15 65.2 5 21 AAY97951 Endothelin recepto
 92 15 65.2 5 21 AAY97952 Endothelin recepto
 93 15 65.2 5 21 AAY85099 HBV surface antige
 94 15 65.2 5 21 AAY85100 HBV surface antige
 95 15 65.2 5 21 AAY85101 HBV surface antige
 96 15 65.2 5 21 AAY85102 HBV surface antige
 97 15 65.2 5 21 AAY85103 HBV surface antige
 98 15 65.2 5 21 AAY89380 Core polypeptide f
 99 15 65.2 5 22 AAM47406 Peptide #36 for il
 100 15 65.2 5 22 ABB00788 Viral DPI78/107-11

ALIGNMENTS

RESULT 1
 AAY33038

ID AAY33038 standard; peptide; 5 AA.

XX AC AAY33038;

XX 03-NOV-1999 (first entry)

XX DE Carbohydrate antigen peptide mimotope 11.

XX Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;
 KW tumour immunity; cancer therapy; antibacterial; immune response;
 KW immunogenicity; anti-idiotype; T cell response manipulation.

XX Synthetic.

XX WO9940433-A1.

XX 12-AUG-1999.

XX 04-FEB-1999; 99WO-US02405.

XX 04-FEB-1998; 98US-0073690.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Kieber-Emmons T;

XX WPI; 1999-527317/44.

XX Peptides and recombinant antibody mimics of carbohydrate antigens,
 PT used for, e.g. treatment of cancer and infection

XX Claim 21; Page 72; 88pp; English.

XX This invention describes a novel method for preparing a peptide or
 CC recombinant antibody, which mimics an antigenic carbohydrate. The
 CC peptides and recombinant antibodies prepared to mimic antigenic
 CC carbohydrates can be used to enhance binding of anti-antigenic
 CC carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine
 CC adjuvants. The peptides can be used to inhibit binding of a ligand to a
 CC receptor, which is an antigenic carbohydrate. The methods are used to
 CC prepare the peptides and antigenic antibodies, which mimic the antigenic
 CC carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour
 CC immunity and cancer therapy. The peptides and antibodies can also be
 CC used as antibacterials. Peptides that mimic carbohydrate antigens can be
 CC formulated to develop a longer lasting immune response. Other advantages
 CC of the peptide mimics are; (1) the chemical composition and purity of
 CC synthesized peptides can be precisely defined; (2) the immunogenicity
 CC of the peptides can be significantly enhanced by polymerization or
 CC addition of relatively small carrier molecules that reduce the total

CC amount of antigen required for immunization; (3) peptide synthesis may
 CC be more practical than synthesis of carbohydrate-protein conjugates or
 CC the production of anti-idiotypes; (4) peptide mimicking sequences can
 CC be engineered into DNA plasmids for DNA vaccination to further
 CC manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate
 CC antigen peptide mimotopes described in the invention.

XX SQ Sequence 5 AA;

Query Match 87.0%; Score 20; DB 20; Length 5;

Best Local Similarity 60.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXLLW 5

Db 1 FSLLW 5

RESULT 2

AAB07280

ID AAB07280 standard; peptide; 5 AA.

XX AC AAB07280;

XX 17-OCT-2000 (first entry)

XX Motif binding to anti-Lewis antigen antibody BR55-2.

XX Human; peptido-mimetic; tumour metastasis; E-selectin;
 KW adhesion molecule; Lewis antigen; anti-adhesion therapy.

XX Unidentified.

XX WO200027420-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US26277.

XX 06-NOV-1998; 98US-0107478.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Blaszczyk-Thurin M, Kieber-Emmons T;

XX WPI; 2000-376309/32.

XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating
 PT inflammation, metastasis and angiogenesis -

XX Example 5; Page 37; 107pp; English.

XX Tumour metastasis requires detachment of malignant cells from the primary
 CC tumour, penetration of blood or lymph vessels and attachment to the
 CC endothelium of distant organs, ultimately resulting in the formation of
 CC new tumours. The selectin family of adhesion molecules is implicated in
 CC this process. E-selectin is a calcium-dependent molecule expressed by
 CC activated vascular endothelium. E-selectins bind to glycoconjugates
 CC carrying a terminal tetrasaccharide Lewis antigen, which are found on
 CC tumour cell surfaces. One such Lewis antigen is Lewis Y (LeY). The
 CC binding of selectin molecules to their ligands is thought to be an
 CC important step in metastasis. Therefore, inhibition of
 CC E-selectin-dependent carbohydrate-mediated interactions is thought to
 CC be a target for anti-cancer therapy. The present sequence is a non
 CC planar-X-planar type motif. This motif is thought to bind to anti-LeY
 CC antibody BR55-2. BR55-2 is a peptido-mimetic of E-selectins. Peptides
 CC that block E-selectin-LeY binding and therefore adhesion of tumour cells
 CC and leukocytes to endothelial cells inhibit metastasis.

XX SQ Sequence 5 AA;

Query Match 87.0%; Score 20; DB 21; Length 5;

Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| | | | |
Db 1 FSLWL 5

RESULT 3
AAW17808
ID AAW17808 standard; peptide; 5 AA.
XX
AC AAW17808;
XX
DT 07-JUL-1997 (first entry)
XX
DE Cyclic pentapeptide #24 used in LH-RH receptor antagonist.
XX
KW Luteinising hormone releasing hormone receptor; LH-RH; antagonist;
KW sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
KW breast; pituitary; prostatic; endometriosis; hysteromyoma;
KW precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
KW multilocular ovarian syndrome; comedo; pregnancy; contraception;
KW ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
KW fish; testosterone; superagonist; leuporelin acetate.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Joined via a peptide linkage to Trp5"
FT Modified-site 2 /note= "N-pToluenesulphonylarginine, D-form residue"
FT Misc-difference 4 /note= "D-form residue"
FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"
FT
FT
FT
XX
OS Synthetic.
XX
XX WO9634012-A1.
PN
XX 31-OCT-1996.
PD
XX
XX 25-APR-1996; 96WO-JP01140.
PF
XX
XX 09-MAY-1995; 95JP-0110933.
PR
XX 28-APR-1995; 95JP-0106775.
PR
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX
XX Furuya S, Kato K, Kitada C;
PI
XX WPI; 1996-497569/49.
DR
XX
XX Cyclic penta-peptide(s), some new, as LH-RH receptor antagonists -
PT used to treat or prevent sex hormone dependent disorders, e.g.
PT cancer, also for control of pregnancy and menstruation and to
PT improve meat quality in animals
XX
XX Example 44; Page 172; 198pp; English.
PS
XX
XX This peptide represents a cyclic peptide which is included in the
CC luteinising hormone releasing hormone (LH-RH) receptor antagonist
CC composition of the invention. Peptides such as this are used to
CC prevent or treat sex-hormone dependent disorders in human or veterinary
CC medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
CC prostatic, endometriosis, hysteromyoma or precocious puberty, but
CC also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
CC comedo, etc.; also to control pregnancy (contraception for men or women,
CC also to induce ovulation) and the menstrual cycle. They are also used
CC to control oestrus in animals, to improve meat quality and control
CC growth, and to promote spawning in fish. They may also inhibit the
CC transient increase in testosterone blood levels caused by admin. of
CC superagonists such as leuporelin acetate.

Query Match 82.6%; Score 19; DB 17; Length 5;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| | | | |
Db 1 FFLWL 5

RESULT 4
AAR89911
ID AAR89911 standard; peptide; 5 AA.
XX
AC AAR89911;
XX
DT 10-SEP-1996 (first entry)
XX
DE p53/MDM2 binding inhibitor #1.
XX
KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
KW inhibition; diagnosis; treatment; malignancy; consensus.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 2 /note= Any amino acid
FT Misc-difference 3 /note= Any amino acid
FT
XX WO9602642-A1.
PN
XX 01-FEB-1996.
PD
XX
XX 20-JUL-1995; 95WO-GB01719.
PF
XX
XX 19-APR-1995; 95US-0424957.
PR
XX 20-JUL-1994; 94US-0277660.
PR
XX (UYDU-) UNIV DUNDEE.
PA
XX
XX Lane DP, Pickesley SM;
PI
XX WPI; 1996-105905/11.
DR
XX
XX New cpds. which interfere with binding of MDM2 and p53 - used to
PT develop prods. for use in the diagnosis and treatment of cancer and
PT other malignancies
PT
XX
XX Claim 4; Page 29; 46pp; English.
PS
XX
XX New peptides of the invention which interfere with the binding of the
CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
CC the peptide sequences AAR89911-3 which form part of the p53 protein
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX
SQ Sequence 5 AA;

Query Match 82.6%; Score 19; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
| | | | |
Db 1 FXXLW 5

```

RESULT 5
AAR89912
ID AAR89912 standard; peptide; 5 AA.
AC AAR89912;
XX
DT 10-SEP-1996 (first entry)
XX
DE p53/MDM2 binding inhibitor #2.
XX
XX Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
KW inhibition; diagnosis; treatment; malignancy; consensus.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Misc-difference 2 /note= Any amino acid
XX
XX WO9602642-A1.
PN
XX
XX 01-FEB-1996.
PD
XX
XX 20-JUL-1995; 95WO-GB01719.
PF
XX
XX 19-APR-1995; 95US-0424957.
PR
XX 20-JUL-1994; 94US-0277660.
XX
XX (UYDU-) UNIV DUNDEE.
PA
XX
XX Lane DP, Picksley SM;
PI
XX
XX WPI; 1996-105905/11.
DR
XX
XX New cpds. which interfere with binding of MDM2 and p53 - used to
PT develop prods. for use in the diagnosis and treatment of cancer and
PT other malignancies
PT
XX
XX Claim 5; Page 29; 46pp; English.
PS
XX
XX New peptides of the invention which interfere with the binding of the
CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
CC the peptide sequences AAR89911-3 which form part of the p53 protein
CC binding motif between amino acids 16-33 (AAR89914). The peptides were
CC identified by modifying the p53 consensus binding sequence by
CC substitution of an Alanine at each pos. and identifying which amino
CC acid changes altered binding to expressed MDM2. The peptides and
CC methods of identifying similar inhibitory peptides can be used to
CC diagnose and treat e.g. cancer and other malignancies.
XX
XX Sequence 5 AA;
QY
Query Match 82.6%; Score 19; DB 17; Length 5;
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 FXXLW 5
DB 1 FXELW 5
RESULT 6
AAY58280
ID AAY58280 standard; peptide; 5 AA.
XX
XX AAY58280;
AC
XX
XX 27-MAR-2000 (first entry)
DT
XX
XX Human p53 consensus hydrophobic interaction motif.
DE
XX

```

```

KW Nuclear receptor; p160 coactivator; NR-box; coactivator binding domain;
KW NR; AF2 transactivation domain; wild-type; thyroid hormone receptor; TR;
KW retinoid receptor; RAR; RXR; peroxisome receptor; PPAR;
KW vitamin D receptor; VDR; oestrogen receptor; ER; glucocorticoid receptor;
KW GR; progesterin receptor; PR; mineralocorticoid receptor; MR;
KW androgen receptor; AR; Grip-1; Tif2; NcoA-2; RAC3; AIB1; TRAM-1; P/CIP;
KW SRC1; breast cancer; prostate cancer; cardiac arrhythmia; infertility;
KW osteoporosis; hyperthyroidism; hypercholesterolaemia; obesity;
KW protein_coordinates.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
PH Misc-difference 2 /label= Xaa
FT /note= "Xaa = any amino acid"
FT
FT Misc-difference 3 /label= Xaa
FT /note= "Xaa = any amino acid"
XX
XX WO9960014-A2.
PN
XX
XX 25-NOV-1999.
PD
XX
XX 30-MAR-1999; 99WO-US06899.
PF
XX
XX 30-MAR-1998; 98US-0079956.
PR
XX 16-DEC-1998; 98US-0113146.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Baxter JD, Darimont B, Feng W, Fletterick R, Kushner FJ;
PI Wagner RL, West BL, Yamamoto KR;
XX
XX WPI; 2000-072429/06.
DR
XX
XX Identifying modulators of nuclear receptor coactivator binding useful
PT for generating new compounds which distinguish nuclear receptor
PT isoforms -
PT
XX
XX Example 14B; Page 12; 281pp; English.
PS
XX
XX The invention relates a method of identification of a compound that
CC modulates coactivator binding to a nuclear receptor. The method
CC comprises modelling test compounds that fit spatially into a nuclear
CC receptor (NR) coactivator binding site of interest using an atomic
CC structural model of a nuclear receptor coactivator binding site. The
CC test compounds are screened by their ability to bind to an NR
CC coactivator binding site, leading to the identification of a compound
CC which modulates coactivator binding. Nuclear receptors are a superfamily
CC of hormone/ ligand activated transcription factors, and includes thyroid
CC hormone receptors (TRs), retinoid receptors (RARS and RXRS), peroxisome
CC receptors (PPARs and XPARs), vitamin D receptors (VDRs), oestrogen
CC receptors (ERs), glucocorticoid receptors (GRs), progesterin receptors
CC (PRs), mineralocorticoid receptors (MRs), androgen receptors (ARs) and
CC icosanoid receptors (IRs). These receptors, in addition to binding their
CC cognate ligand, also bind coactivator proteins that are involved in
CC receptor function, for example NRs can stimulate transcription in
CC response to hormone binding by recruiting coactivator proteins to the
CC promoters of responsive genes. Coactivators of the p160 family mediate
CC activity of a transcriptional activation domain, AF2, that is part of the
CC nuclear receptor's ligand binding domain. The method may be used to
CC identify an agonist or antagonist of coactivator binding to a nuclear
CC receptor. The methods can also be used to identify residues which
CC comprise a coactivator binding site of a nuclear receptor of interest.
CC The methods are applicable to generating new compounds that distinguish
CC nuclear receptor isoforms. This can facilitate generation of either
CC tissue- specific or function-specific compounds. Nuclear receptors have
CC been implicated in a variety of medical disorders, including breast
CC cancer, prostate cancer, cardiac arrhythmia, infertility, osteoporosis,
CC hyperthyroidism, hypercholesterolaemia and obesity. Sequences AAY58282-
CC AAY58302 represent the regions (NR-boxes 1-3) of p160 coactivator
CC proteins which interact with the nuclear receptor coactivator binding

```

CC sites (AAV58307-Y58328). The NR coactivator binding sites comprise two
 CC regions of the NR; Helices 3-6 (H3-H6), and helix 12 (H12). The
 CC coactivator NR-boxes all share a consensus sequence LXXLL (AAV58278),
 CC with the NR-box 2 motifs sharing the consensus motif ILXXLL (AAV58279).
 CC Sequences AAV58280-Y58281 represent the hydrophobic interaction motifs of
 CC p53 and VP16 used in an exemplification of the invention. Sequences
 CC AAV58329-Y58240 represent mutant versions of the human Grip-1 NR-box 2
 CC sequence (AAV58283), and sequences AAV58341-Y58353 represent mutant
 CC versions of NR coactivator binding sites, used in exemplifications of the
 CC invention.
 XX
 SQ Sequence 5 AA;

Query Match 82.6%; Score 19; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
 |||||
 DB 1 FXXLW 5

RESULT 7
 AAO20822
 ID AAO20822 standard; Peptide; 5 AA.

AC AAO20822;

XX
 XX
 DT 08-JUL-2002 (first entry)

DE Hydrophobic interaction FxxLW motif of p53.

XX Cytostatic; cardiovascular; antiarrhythmic; vasotropic; osteopathic;
 KW endocrinal; antilipaeamic; anorectic; coactivator binding; lead compound;
 KW nuclear receptor; NR; BS; peptidomimetic; scaffold; breast cancer;
 KW nuclear receptor-based disorder; prostate cancer; cardiac arrhythmia;
 KW infertility; osteoporosis; hyperthyroidism; hypercholesterolaemia;
 KW obesity; FxxLW motif; p53; Glucocorticoid; GR; protein co-ordinate data.
 XX
 OS Unidentified.

Key Location/Qualifiers
 FT Misc-difference 2 /label= unknown
 FT /note= "Xaa is unknown"
 FT Misc-difference 3 /label= unknown
 FT /note= "Xaa is unknown"

XX WO200202488-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US20969.

XX 30-JUN-2000; 2000US-0609361.

XX (REGC) UNIV CALIFORNIA.

XX Guy RK, Baxter JD, Darimont B, Feng W, Fletterick RJ, Kushner PJ;
 PI Wagner RL, West BL, Yamamoto KR, Geistlinger TR, Arnold JR;
 PI Kuntz ID;

XX WPI; 2002-315164/35.

XX Method for identifying agonist and antagonist compounds used for
 PT modulating nuclear receptor coactivator binding, which are useful in
 PT treating nuclear receptor-based disorders e.g. breast cancer,
 PT infertility, or hyperthyroidism -

XX Example 14; Page 15; 307pp; English.

XX The invention relates to a method for identifying a compound that

CC modulates coactivator binding to a nuclear receptor (NR). The method
 CC comprises modelling test compounds that fit electrostatically into an NR
 CC coactivator binding site (BS) using an appropriate atomic structural
 CC model of (BS); screening the test compounds in an assay characterised by
 CC binding of a test compound to (BS); and identifying a library or test
 CC compound that modulates coactivator binding to the NR. The methods of the
 CC invention are useful for identifying peptides, peptidomimetics, or small
 CC natural or synthetic organic molecules that modulate nuclear receptor
 CC activity, particularly new lead compounds, scaffolds and combinatorial
 CC libraries. The methods are used in selecting and characterising structure
 CC /function relationships of natural or synthetic coactivator compounds,
 CC which are useful in treating nuclear receptor-based disorders e.g. breast
 CC cancer, prostate cancer, cardiac arrhythmia, infertility, osteoporosis,
 CC hyperthyroidism, hypercholesterolaemia or obesity. This sequence
 CC represents the hydrophobic interaction FxxLW motif of p53. The
 CC glucocorticoid (GR) nuclear receptor of the invention is able to interact
 CC with peptides containing this motif.
 XX
 SQ Sequence 5 AA;

Query Match 82.6%; Score 19; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
 |||||
 DB 1 FXXLW 5

RESULT 8
 AAR29438

ID AAR29438 standard; peptide; 5 AA.

XX AAR29438;

DT 13-APR-1993 (first entry)

DE Endothelin antagonist peptide.

XX Hypertension; myocardial infarction; congestive heart failure;
 KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
 KW acute renal failure; pre-eclampsia; diabetes; metabolic;
 KW endocrinological; neurological; disorders.

XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 1 /note= " (Ac- or 1-adamantyl acetic acid) - D-Phe"

XX WO9220706-A.

XX 26-NOV-1992.

XX 24-APR-1992; 92WO-US03408.

XX 16-MAY-1991; 91US-0701274.

XX 18-DEC-1991; 91US-0809746.

XX (WARN) WARNER LAMBERT CO.

XX Cody WL, Depue P, Doherty AM, Taylor MD;

XX WPI; 1992-415706/50.

XX New peptide(s) used as endothelin antagonists - for treating
 PT hypertension, metabolic and endocrine disorders, heart failure,
 PT diabetes, asthma, neurological disorders, etc.

XX Claim 5; Page 94; 116pp; English.

XX The peptide is an endothelin antagonist useful in controlling
 CC hypertension, myocardial infarction, congestive heart failure,

CC endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
CC acute renal failure, preclampsia, diabetes and metabolic,
CC endocrinological and neurological disorders. Administration is oral
CC parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
CC day. It may be prepared by conventional peptide synthesis.
XX
SQ Sequence 5 AA;

Query Match 73.9%; Score 17; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLM 5
Db 1 FDIW 5

RESULT 9
AAR29448
ID AAR29448 standard; peptide; 5 AA.
XX
AC AAR29448;
XX
DT 13-APR-1993 (first entry)
XX
DE Endothelin antagonist peptide.
XX
KW Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preclampsia; diabetes; metabolic;
KW endocrinological; neurological; disorders.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Ac-D-Phe"
XX
XX WO9220706-A.
XX
PD 26-NOV-1992.
XX
XX 24-APR-1992; 92WO-US03408.
XX
XX 16-MAY-1991; 91US-0701274.
XX
PR 18-DEC-1991; 91US-0809746.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Cody WL, Depue P, Doherty AM, Taylor MD;
XX WPI; 1992-415706/50.
XX
XX New peptide(s) used as endothelin antagonists - for treating
XX hypertension, metabolic and endocrine disorders, heart failure,
XX diabetes, asthma, neurological disorders, etc.
XX
XX Claim 5; Page 95; 116pp; English.
XX
XX The peptide is an endothelin antagonist useful in controlling
XX hypertension, myocardial infarction, congestive heart failure,
XX endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
XX acute renal failure, preclampsia, diabetes and metabolic,
XX endocrinological and neurological disorders. Administration is oral
XX parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
XX day. It may be prepared by conventional peptide synthesis.
XX
SQ Sequence 5 AA;

Query Match 73.9%; Score 17; DB 13; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLM 5
Db 1 FDIW 5

RESULT 9
AAR29448
ID AAR29448 standard; peptide; 5 AA.
XX
AC AAR29448;
XX
DT 13-APR-1993 (first entry)
XX
DE Endothelin antagonist peptide.
XX
KW Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preclampsia; diabetes; metabolic;
KW endocrinological; neurological; disorders.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Ac-D-Phe"
XX
XX WO9220706-A.
XX
PD 26-NOV-1992.
XX
XX 24-APR-1992; 92WO-US03408.
XX
XX 16-MAY-1991; 91US-0701274.
XX
PR 18-DEC-1991; 91US-0809746.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Cody WL, Depue P, Doherty AM, Taylor MD;
XX WPI; 1992-415706/50.
XX
XX New peptide(s) used as endothelin antagonists - for treating
XX hypertension, metabolic and endocrine disorders, heart failure,
XX diabetes, asthma, neurological disorders, etc.
XX
XX Claim 5; Page 95; 116pp; English.
XX
XX The peptide is an endothelin antagonist useful in controlling
XX hypertension, myocardial infarction, congestive heart failure,
XX endotoxic shock, subarachnoid haemorrhage, asthma, arrhythmias,
XX acute renal failure, preclampsia, diabetes and metabolic,
XX endocrinological and neurological disorders. Administration is oral
XX parenteral or by inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/
XX day. It may be prepared by conventional peptide synthesis.
XX
SQ Sequence 5 AA;

QY 1 FXXLM 5
Db 1 FDIW 5

RESULT 10
AAR69220
ID AAR69220 standard; peptide; 5 AA.
XX
AC AAR69220;
XX
DT 06-MAR-1995 (first entry)
XX
DE Endothelin C-terminal peptide analog, useful as antagonist.
XX
KW Endothelin; ET-1; receptor; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Ac-D-Phe"
XX
XX WO9414843-A.
XX
PD 07-JUL-1994.
XX
XX 17-DEC-1993; 93WO-US12377.
XX
PR 21-DEC-1992; 92US-0995480.
XX
XX (WARN) WARNER LAMBERT CO.
XX
XX Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
XX WPI; 1994-234617/28.
XX
XX New hexapeptide derivs. inhibiting endothelin - for treatment of
XX e.g. renal failure, hypertension, asthma, restenosis, angina,
XX cancer etc.
XX
XX Claim 5; Page 119; 146pp; English.
XX
XX Novel antagonists of endothelin are claimed which are C-terminal
XX hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
XX of the new peptides has D-configuration. The peptides are claimed
XX generically. The present peptide is a specifically claimed example
XX of the generic compounds.
XX The peptides are useful for treating hypertension, metabolic and
XX endocrine disorders, congestive heart failure, myocardial infarction,
XX endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
XX and chronic renal failure, preclampsia, diabetes, neurological
XX disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
XX disease, gastric mucosal damage, Raynaud's disease, restenosis,
XX percutaneous transluminal coronary angioplasty, angina and cancer.
XX
SQ Sequence 5 AA;

Query Match 73.9%; Score 17; DB 15; Length 5;
Best Local Similarity 40.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLM 5
Db 1 FDIW 5

RESULT 11
AAR69260
ID AAR69260 standard; peptide; 5 AA.
XX
AC AAR69260;
XX

DT 07-MAR-1995 (first entry)
 XX Endothelin C-terminal peptide analog, useful as antagonist.
 XX Endothelin; ET-1; receptor; antagonist.
 KW Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Ac-D-Phe"
 XX
 XX WO9414843-A.
 PN
 XX
 PD 07-JUL-1994.
 XX
 PF 17-DEC-1993; 93WO-US12377.
 XX
 PR 21-DEC-1992; 92US-0995480.
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX
 PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
 XX WPI; 1994-234617/28.
 DR
 XX
 PF New hexa-peptide derivs. inhibiting endothelin - for treatment of
 XX e.g. renal failure, hypertension, asthma, restenosis, angina,
 PT cancer etc.
 FT
 XX
 PS Claim 5; Page 120; 146pp; English.
 XX
 CC Novel antagonists of endothelin are claimed which are C-terminal
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
 CC of the new peptides has D-configuration. The peptides are claimed
 CC generically. The present peptide is a specifically claimed example
 CC of the generic compounds.
 CC The peptides are useful for treating hypertension, metabolic and
 CC endocrine disorders, congestive heart failure, myocardial infarction,
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
 CC and chronic renal failure, preclampsia, diabetes, neurological
 CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
 CC percutaneous transluminal coronary angioplasty, angina and cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 73.9%; Score 17; DB 15; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXLW 5
 | : |
 Db 1 FDFIW 5
 RESULT 12
 AAR69210
 ID AAR69210 standard; peptide; 5 AA.
 XX
 AC AAR69210;
 XX
 DT 06-MAR-1995 (first entry)
 XX
 DE Endothelin C-terminal peptide analog, useful as antagonist.
 XX Endothelin; ET-1; receptor; antagonist.
 KW Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Ac-D-Phe or Ada-D-Phe, where Ada is

FT 1-adamantyl-acetyl"
 XX WO9414843-A.
 PN
 XX
 PD 07-JUL-1994.
 XX
 PF 17-DEC-1993; 93WO-US12377.
 XX
 PR 21-DEC-1992; 92US-0995480.
 XX
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX
 PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
 XX WPI; 1994-234617/28.
 DR
 XX
 PF New hexa-peptide derivs. inhibiting endothelin - for treatment of
 XX e.g. renal failure, hypertension, asthma, restenosis, angina,
 PT cancer etc.
 FT
 XX
 PS Claim 5; Page 118; 146pp; English.
 XX
 CC Novel antagonists of endothelin are claimed which are C-terminal
 CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid
 CC of the new peptides has D-configuration. The peptides are claimed
 CC generically. The present peptide is a specifically claimed example
 CC of the generic compounds.
 CC The peptides are useful for treating hypertension, metabolic and
 CC endocrine disorders, congestive heart failure, myocardial infarction,
 CC endotoxic shock, subarachnoid haemorrhage, arrhythmia, asthma, acute
 CC and chronic renal failure, preclampsia, diabetes, neurological
 CC disorders, pulmonary hypertension, ischaemic disease, ischaemic bowel
 CC disease, gastric mucosal damage, Raynaud's disease, restenosis,
 CC percutaneous transluminal coronary angioplasty, angina and cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 73.9%; Score 17; DB 15; Length 5;
 Best Local Similarity 40.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXLW 5
 | : |
 Db 1 FDFIW 5
 RESULT 13
 AAR13339
 ID AAR13339 standard; peptide; 5 AA.
 XX
 AC AAR13339;
 XX
 DT 22-OCT-1991 (first entry)
 XX
 DE Endothelin antagonist peptide WS 7338.
 XX
 KW Cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /label= D-allo, D-Val
 FT Modified-site 3
 FT /label= D-Trp
 FT Modified-site 4
 FT /label= D-Glu
 XX
 PN JP03130299-A.
 XX
 PD 04-JUN-1991.
 FT
 XX 08-AUG-1990; 90JP-0212952.

XX	31-AUG-1989;	89GB-0019726.
PR	(FUJI) FUJISAWA PHARM KK.	
XX	WPI; 1991-241129/33.	
XX	New peptide prepd. by culturing Streptomyces spp - used as	
PT	endothelin antagonist.	
XX	Claim 1; page 1; 15pp; Japanese.	
PS	The peptide is prepd. by cyclisation of the synthetic peptide.	
XX	The Trp residue at posn. 3 may be side chain protected with a lower	
CC	alkanoyl gp; the Glu residue at posn. 4 may be protected with an	
CC	al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be	
CC	isolated from cultures of Streptomyces sp. no. 7338.	
CC	See also AAR13909 and AAR14025.	
XX		
SQ	Sequence 5 AA;	
Query Match	65.2%; Score 15; DB 12; Length 5;	
Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
Matches 2; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 LW 5	
DB	2 LW 3	
RESULT 14		
AAR14025		
ID	AAR14025 standard; peptide; 5 AA.	
XX	AAR14025;	
AC		
XX	22-OCT-1991 (first entry)	
DT	Endothelin antagonist peptide.	
DE	Cyclic.	
XX	Synthetic.	
OS		
XX	Key Location/Qualifiers	
PH	Modified-site 1 /label= D-Val	
FT	Modified-site 3 /label= D-Trp	
FT	Modified-site 4 /label= D-Glu	
FT		
FT		
XX	JP03130299-A.	
PX	04-JUN-1991.	
XX	08-AUG-1990; 90JP-0212952.	
PF		
XX	31-AUG-1989; 89GB-0019726.	
PR	(FUJI) FUJISAWA PHARM KK.	
XX	WPI; 1991-241129/33.	
XX	New peptide prepd. by culturing Streptomyces spp - used as	
PT	endothelin antagonist.	
XX	Claim 1; page 1; 15pp; Japanese.	
PS	The peptide is prepd. by cyclisation of the synthetic peptide.	
XX	The Trp residue at posn. 3 may be side chain protected with a lower	
CC	alkanoyl gp; the Glu residue at posn. 4 may be protected with an	
CC	al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be	
CC	isolated from cultures of Streptomyces sp. no. 7338.	
CC	See also AAR13909 and AAR14025.	
XX		
SQ	Sequence 5 AA;	
Query Match	65.2%; Score 15; DB 12; Length 5;	
Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
Matches 2; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 LW 5	
DB	2 LW 3	
RESULT 14		
AAR14025		
ID	AAR14025 standard; peptide; 5 AA.	
XX	AAR14025;	
AC		
XX	22-OCT-1991 (first entry)	
DT	Endothelin antagonist peptide.	
DE	Cyclic.	
XX	Synthetic.	
OS		
XX	Key Location/Qualifiers	
PH	Modified-site 1 /label= D-Alle	
FT	Modified-site 3 /label= D-Trp	
FT	Modified-site 4 /label= D-Glu	
FT		
FT		
XX	JP03130299-A.	
PX	04-JUN-1991.	
XX	08-AUG-1990; 90JP-0212952.	
PF		
XX	31-AUG-1989; 89GB-0019726.	
PR	(FUJI) FUJISAWA PHARM KK.	
XX	WPI; 1991-241129/33.	
XX	New peptide prepd. by culturing Streptomyces spp - used as	
PT	endothelin antagonist.	
XX	Claim 1; page 1; 15pp; Japanese.	
PS	The peptide is prepd. by cyclisation of the synthetic peptide.	
XX	The Trp residue at posn. 3 may be side chain protected with a lower	
CC	alkanoyl gp; the Glu residue at posn. 4 may be protected with an	
CC	al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be	
CC	isolated from cultures of Streptomyces sp. no. 7338.	
CC	See also AAR13909 and AAR14025.	
XX		
SQ	Sequence 5 AA;	
Query Match	65.2%; Score 15; DB 12; Length 5;	
Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
Matches 2; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 LW 5	
DB	2 LW 3	
RESULT 14		
AAR14025		
ID	AAR14025 standard; peptide; 5 AA.	
XX	AAR14025;	
AC		
XX	22-OCT-1991 (first entry)	
DT	Endothelin antagonist peptide.	
DE	Cyclic.	
XX	Synthetic.	
OS		
XX	Key Location/Qualifiers	
PH	Modified-site 1 /label= D-Alle	
FT	Modified-site 3 /label= D-Trp	
FT	Modified-site 4 /label= D-Glu	
FT		
FT		
XX	JP03130299-A.	
PX	04-JUN-1991.	
XX	08-AUG-1990; 90JP-0212952.	
PF		
XX	31-AUG-1989; 89GB-0019726.	
PR	(FUJI) FUJISAWA PHARM KK.	
XX	WPI; 1991-241129/33.	
XX	New peptide prepd. by culturing Streptomyces spp - used as	
PT	endothelin antagonist.	
XX	Claim 1; page 1; 15pp; Japanese.	
PS	The peptide is prepd. by cyclisation of the synthetic peptide.	
XX	The Trp residue at posn. 3 may be side chain protected with a lower	
CC	alkanoyl gp; the Glu residue at posn. 4 may be protected with an	
CC	al (lower) alkyl gp. An analogous natural peptide, WS 7338, may be	
CC	isolated from cultures of Streptomyces sp. no. 7338.	
CC	See also AAR13909 and AAR14025.	
XX		
SQ	Sequence 5 AA;	
Query Match	65.2%; Score 15; DB 12; Length 5;	
Best Local Similarity	100.0%; Pred. No. 7.8e+05;	
Matches 2; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	4 LW 5	
DB	2 LW 3	
RESULT 14		
AAR14025		
ID	AAR14025 standard; peptide; 5 AA.	
XX	AAR14025;	
AC		
XX	22-OCT-1991 (first entry)	
DT	Endothelin antagonist peptide.	
DE	Cyclic.	
XX	Synthetic.	
OS		
XX	Key Location/Qualifiers	
PH	Modified-site 1 /label= D-Alle	
FT	Modified-site 3 /label= D-Trp	
FT	Modified-site 4 /label= D-Glu	
FT		
FT		
XX	JP03130299-A.	
PX	04-JUN-1991.	
XX	08-AUG-1990; 90JP-0212952.	
PF		
XX	31-AUG-1989; 89GB-0019726.	
PR	(FUJI) FUJISAWA PHARM KK.	
XX	WPI;	


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ID  AAR38437 standard; peptide; 5 AA.
XX  AAR38437;
AC
XX
DT  07-MAR-1994 (first entry)
XX
DE  Endothelin receptor antagonist peptide #2.
XX
KW  Cyclic; endothelin receptor; antagonist; cardiac disease;
KW  myocardial infarction; acute renal insufficiency; asthma.
XX
XX  OS
XX
XX  Key
XX  Location/Qualifiers
FH  Misc-difference 1
FT  /note= "D-form residue"
FT  Misc-difference 2
FT  /label= OTHER
FT  /note= "alpha-Abu, delta-Ava or epsilon-Aca"
FT  Misc-difference 3
FT  /note= "D-form residue"
FT  Misc-difference 5
FT  /note= "D-form residue"
FT  /note= "D-form residue"
PN  JP05194589-A.
XX
XX  PD
XX  03-AUG-1993.
XX
XX  30-JUN-1992; 92JP-0173065.
XX
XX  31-JUL-1991; 91JP-0191454.
XX
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX
XX  WPI; 1993-282913/36.
XX
XX  Novel cyclic peptide(s) used as endothelin receptor antagonists -
XX  for treating cardiac diseases, e.g. myocardial infarction, acute
XX  renal insufficiency or asthma
XX
XX  Example 4-6; Page 6; 8pp; Japanese.
XX
XX  The sequences given in AAR38436-38 are cyclic peptides which act as
XX  endothelin receptor antagonists. They may be used in the treatment
XX  of cardiac disease, acute renal insufficiency or asthma.
XX
XX  Sequence 5 AA;
SQ
XX
XX  Query Match
XX  Best Local Similarity 65.2%; Score 15; DB 14; Length 5;
XX  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 4 LW 5
XX  ||
XX  Db 4 LW 5
XX
XX  RESULT 17
XX  AAR38438
XX  ID AAR38438 standard; peptide; 5 AA.
XX
XX  AC AAR38438;
XX
XX  DT 07-MAR-1994 (first entry)
XX
XX  DE Endothelin receptor antagonist peptide #3.
XX
XX  KW Cyclic; endothelin receptor; antagonist; cardiac disease;
XX  KW myocardial infarction; acute renal insufficiency; asthma.
XX
XX  OS Synthetic.
XX
XX  Key
XX  Location/Qualifiers
FH  Misc-difference 1
FT  /note= "D-form residue"
FT  Misc-difference 2
FT  /label= OTHER
FT  /note= "alpha-Abu, delta-Ava or epsilon-Aca"
FT  Misc-difference 3
FT  /note= "D-form residue"
FT  Misc-difference 5
FT  /note= "D-form residue"
PN  JP05194589-A.
XX
XX  PD
XX  03-AUG-1993.
XX
XX  30-JUN-1992; 92JP-0173065.
XX
XX  31-JUL-1991; 91JP-0191454.
XX
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX
XX  WPI; 1993-282913/36.
XX
XX  Novel cyclic peptide(s) used as endothelin receptor antagonists -
XX  for treating cardiac diseases, e.g. myocardial infarction, acute
XX  renal insufficiency or asthma
XX
XX  Example 4-6; Page 6; 8pp; Japanese.
XX
XX  The sequences given in AAR38436-38 are cyclic peptides which act as
XX  endothelin receptor antagonists. They may be used in the treatment
XX  of cardiac disease, acute renal insufficiency or asthma.
XX
XX  Sequence 5 AA;
SQ
XX
XX  Query Match
XX  Best Local Similarity 65.2%; Score 15; DB 14; Length 5;
XX  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 4 LW 5
XX  ||
XX  Db 4 LW 5
XX
XX  RESULT 18
XX  AAR38436
XX  ID AAR38436 standard; peptide; 5 AA.
XX
XX  AC AAR38436;
XX
XX  DT 07-MAR-1994 (first entry)
XX
XX  DE Endothelin receptor antagonist peptide #1.
XX
XX  KW Cyclic; endothelin receptor; antagonist; cardiac disease;
XX  KW myocardial infarction; acute renal insufficiency; asthma.
XX
XX  OS Synthetic.
XX
XX  Key
XX  Location/Qualifiers
FH  Misc-difference 1
FT  /note= "D-form residue"
FT  Misc-difference 2
FT  /label= OTHER
FT  /note= "alpha-Abu, delta-Ava or epsilon-Aca"
FT  Misc-difference 3
FT  /note= "D-form residue"
FT  Misc-difference 5
FT  /note= "D-form residue"
PN  JP05194589-A.
XX
XX  PD
XX  03-AUG-1993.
XX

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FT  Misc-difference 1
FT  /note= "D-form residue"
FT  Misc-difference 2
FT  /label= OTHER
FT  /note= "beta-Asp"
FT  Misc-difference 3
FT  /note= "D-form residue"
FT  Misc-difference 5
FT  /note= "D-form residue"
XX
XX  JP05194589-A.
XX
XX  PD
XX  03-AUG-1993.
XX
XX  30-JUN-1992; 92JP-0173065.
XX
XX  31-JUL-1991; 91JP-0191454.
XX
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX
XX  WPI; 1993-282913/36.
XX
XX  Novel cyclic peptide(s) used as endothelin receptor antagonists -
XX  for treating cardiac diseases, e.g. myocardial infarction, acute
XX  renal insufficiency or asthma
XX
XX  Disclosure; Page 6; 8pp; Japanese.
XX
XX  The sequences given in AAR38436-38 are cyclic peptides which act as
XX  endothelin receptor antagonists. They may be used in the treatment
XX  of cardiac disease, acute renal insufficiency or asthma.
XX
XX  Sequence 5 AA;
SQ
XX
XX  Query Match
XX  Best Local Similarity 65.2%; Score 15; DB 14; Length 5;
XX  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 4 LW 5
XX  ||
XX  Db 4 LW 5
XX
XX  RESULT 18
XX  AAR38436
XX  ID AAR38436 standard; peptide; 5 AA.
XX
XX  AC AAR38436;
XX
XX  DT 07-MAR-1994 (first entry)
XX
XX  DE Endothelin receptor antagonist peptide #1.
XX
XX  KW Cyclic; endothelin receptor; antagonist; cardiac disease;
XX  KW myocardial infarction; acute renal insufficiency; asthma.
XX
XX  OS Synthetic.
XX
XX  Key
XX  Location/Qualifiers
FH  Misc-difference 1
FT  /note= "D-form residue"
FT  Misc-difference 2
FT  /label= OTHER
FT  /note= "alpha-Abu, delta-Ava or epsilon-Aca"
FT  Misc-difference 3
FT  /note= "D-form residue"
FT  Misc-difference 5
FT  /note= "D-form residue"
PN  JP05194589-A.
XX
XX  PD
XX  03-AUG-1993.
XX

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PF 30-JUN-1992; 92JP-0173065.
 XX
 PR 31-JUL-1991; 91JP-0191454.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-282913/36.
 XX
 XX Novel cyclic peptide(s) used as endothelin receptor antagonists -
 PT for treating cardiac diseases, e.g. myocardial infarction, acute
 PT renal insufficiency or asthma
 XX
 PS Example 1-3; Page 6; 8pp; Japanese.
 XX
 CC The sequences given in AAR38436-38 are cyclic peptides which act as
 CC endothelin receptor antagonists. They may be used in the treatment
 CC of cardiac disease, acute renal insufficiency or asthma.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 4 LW 5

RESULT 19
 AAR35418
 ID AAR35418 standard; peptide; 5 AA.
 XX
 AC AAR35418;
 XX
 DT 03-AUG-1993 (first entry)
 XX
 DE Endothelin receptor inhibitor peptide #1.
 XX
 KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
 KW mammal; myocardial infarction; renal dysfunction; asthma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 XX
 PN JP05059098-A.
 XX
 PD 09-MAR-1993.
 XX
 PF 30-AUG-1991; 91JP-0220610.
 XX
 PR 30-AUG-1991; 91JP-0220610.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-128388/16.
 XX
 XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit
 PT endothelin receptor activity, vasoconstriction etc.; useful for
 PT treating myocardial infarction, acute renal dysfunction and
 PT asthma, etc.
 XX
 PS Example 1; Page 6; 8pp; Japanese.
 XX
 CC The sequences given in AAR35418-28 are cyclic peptides which act as
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive

CC action of endothelin. They are useful as drugs for improving
 CC circulatory function in mammals, in treatment of myocardial
 CC infarction, acute renal dysfunction or asthma. These peptides may
 CC be prepared by conventional methods of solid or aqueous phase
 CC synthesis.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 3 LW 4

RESULT 20
 AAR35419
 ID AAR35419 standard; peptide; 5 AA.
 XX
 AC AAR35419;
 XX
 DT 03-AUG-1993 (first entry)
 XX
 DE Endothelin receptor inhibitor peptide #2.
 XX
 KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
 KW mammal; myocardial infarction; renal dysfunction; asthma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 XX
 PN JP05059098-A.
 XX
 PD 09-MAR-1993.
 XX
 PF 30-AUG-1991; 91JP-0220610.
 XX
 PR 30-AUG-1991; 91JP-0220610.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-128388/16.
 XX
 XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit
 PT endothelin receptor activity, vasoconstriction etc.; useful for
 PT treating myocardial infarction, acute renal dysfunction and
 PT asthma, etc.
 XX
 PS Example 2; Page 7; 8pp; Japanese.
 XX
 CC The sequences given in AAR35418-28 are cyclic peptides which act as
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive
 CC action of endothelin. They are useful as drugs for improving
 CC circulatory function in mammals, in treatment of myocardial
 CC infarction, acute renal dysfunction or asthma. These peptides may
 CC be prepared by conventional methods of solid or aqueous phase
 CC synthesis.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 3 LW 4

RESULT 21

AAR35421
ID AAR35421 standard; peptide; 5 AA.

AC AAR35421;

XX 03-AUG-1993 (first entry)

XX Endothelin receptor inhibitor peptide #4.

KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
KW mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta:peptide derivs. contg. one L-aminoacid - inhibit
XX endothelin receptor activity, vasoconstriction etc., useful for
XX treating myocardial infarction, acute renal dysfunction and
XX asthma, etc.

XX Example 4; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as
XX endothelin inhibitors. They strongly inhibit the vasoconstrictive
XX action of endothelin. They are useful as drugs for improving
XX circulatory function in mammals, in treatment of myocardial
XX infarction, acute renal dysfunction or asthma. These peptides may
XX be prepared by conventional methods of solid or aqueous phase
XX synthesis.

XX Sequence 5 AA;

Query Match

Best Local Similarity 65.2%; Score 15; DB 14; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

DB 3 LW 4

RESULT 22

AAR35422

ID AAR35422 standard; peptide; 5 AA.

AC AAR35422;

XX 03-AUG-1993 (first entry)

XX Endothelin receptor inhibitor peptide #6.

KW Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
KW mammal; myocardial infarction; renal dysfunction; asthma.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "D-form residue"
XX Misc-difference 3

XX

DE

XX

KW

XX

OS

XX

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FT

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FT

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FT

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FT

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PN

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PD

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XX

CC endothelin inhibitors. They strongly inhibit the vasoconstrictive
 CC action of endothelin. They are useful as drugs for improving
 CC circulatory function in mammals, in treatment of myocardial
 CC infarction, acute renal dysfunction or asthma. These peptides may
 CC be prepared by conventional methods of solid or aqueous phase
 CC synthesis.
 XX

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
 ||
 Db 3 LW 4

RESULT 26

AAR35426
 ID AAR35426 standard; peptide; 5 AA.

XX AAR35426;

DT 03-AUG-1993 (first entry)

Endothelin receptor inhibitor peptide #9.

Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
 mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit
 PT endothelin receptor activity, vasoconstriction etc., useful for
 PT treating myocardial infarction, acute renal dysfunction and
 PT asthma, etc.

XX Example 9; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as
 CC endothelin inhibitors. They strongly inhibit the vasoconstrictive
 CC action of endothelin. They are useful as drugs for improving
 CC circulatory function in mammals, in treatment of myocardial
 CC infarction, acute renal dysfunction or asthma. These peptides may
 CC be prepared by conventional methods of solid or aqueous phase
 CC synthesis.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
 ||
 Db 3 LW 4

RESULT 27

AAR35427
 ID AAR35427 standard; peptide; 5 AA.

XX AAR35427;

DT 03-AUG-1993 (first entry)

Endothelin receptor inhibitor peptide #10.

Cyclic; endothelin; inhibitor; vasoconstriction; drug; circulation;
 mammal; myocardial infarction; renal dysfunction; asthma.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

XX JP05059098-A.

XX 09-MAR-1993.

XX 30-AUG-1991; 91JP-0220610.

XX 30-AUG-1991; 91JP-0220610.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1993-128388/16.

XX New cyclic penta-peptide derivs. contg. one L-aminoacid - inhibit

PT endothelin receptor activity, vasoconstriction etc., useful for

PT treating myocardial infarction, acute renal dysfunction and

PT asthma, etc.

XX Example 10; Page 8; 8pp; Japanese.

XX The sequences given in AAR35418-28 are cyclic peptides which act as

CC endothelin inhibitors. They strongly inhibit the vasoconstrictive

CC action of endothelin. They are useful as drugs for improving

CC circulatory function in mammals, in treatment of myocardial

CC infarction, acute renal dysfunction or asthma. These peptides may

CC be prepared by conventional methods of solid or aqueous phase

CC synthesis.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 14; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5

||

Db 3 LW 4

RESULT 28

AAR35428

ID AAR35428 standard; peptide; 5 AA.

XX AAR35428;

XX

DE Cyclic peptide which modulates endothelin activity.

KW Cyclic; peptide; endothelin; inhibitor; receptor; detection;
 XX isolation; antagonist; hypertension; pulmonary hypertension;
 KW cardiovascular disease; bronchoconstriction; asthma;
 KW inflammatory disease; ophthalmologic shock; anaphylactic shock;
 KW haemorrhagic shock; gastroenteric disease; renal failure;
 KW endotoxin shock; menstrual disorders; obstetric conditions;
 KW erythropoietin-mediated vasoconstriction; wound treatment.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-Asp bonded to D-Trp at position 5."
 FT Misc-difference 3 /label= D-His.
 FT Misc-difference 5
 FT /note= "D-Trp bonded to D-Asp at position 1."
 FT
 XX
 PN WO9325580-A.
 XX
 XX 23-DEC-1993.
 PD
 XX
 XX 17-JUN-1993; 93WO-US05788.
 PF
 XX 18-JUN-1992; 92US-0900620.
 PR
 PR 18-JUN-1992; 92US-0900711.
 XX
 PA (IMMU-) IMMUNOPHARMACEUTICS INC.
 XX
 XX Balaji VN, Chan MF;
 PI
 XX WPI; 1994-007458/01.
 DR
 XX New cyclic peptide(s) which modulate endothelin activity - used
 PT for treating endothelin-mediated disorders such as cardiovascular
 PT and respiratory diseases
 PT
 XX
 PS Claim 2; Page 51; 58pp; English.

XX The peptide inhibits binding of endothelin-1 (ET) to ETA receptors
 CC and/or to ETB receptors. It can be used for detecting, peptides
 CC distinguishing and isolating ET receptor subtypes. The peptides
 CC also act as ET antagonists and can be used to treat endothelin-
 CC mediated disorders such as hypertension, pulmonary hypertension,
 CC cardiovascular disease, bronchoconstriction, asthma, inflammatory
 CC diseases, ophthalmologic shock, anaphylactic shock, haemorrhagic
 CC shock, gastroenteric disease, renal failure, endotoxin shock,
 CC menstrual disorders, obstetric conditions, erythropoietin-mediated
 CC vasoconstriction and wounds.

XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 4 LW 5

RESULT 31
 AAR46691
 ID AAR46691 standard; peptide; 5 AA.
 XX
 AC AAR46691;
 XX
 DT 31-AUG-1994 (first entry)
 XX
 DE Monomeric peptide #1, autoimmunogenic in HIV-infected subjects.
 XX
 KW HIV-1; HIV-2; human immunodeficiency virus; AIDS;
 KW acquired immune deficiency syndrome; autoimmune response;

KW immunosuppression; CD4; gp120; T cell activation;
 XX therapy; prophylaxis.

OS Homo sapiens.
 OS Human Immunodeficiency Virus type 1.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "N-terminus is opt. extended
 FT by 1-5 amino acids"
 FT Misc-difference 5 /note= "C-terminus is opt. extended
 FT by 1-5 amino acids"
 FT
 XX WO9403487-A.
 XX
 XX 17-FEB-1994.
 PD
 XX
 XX 10-AUG-1993; 93WO-FR00803.
 PF
 XX 10-AUG-1992; 92FR-0009884.
 PR
 PR 12-FEB-1993; 93FR-0001628.
 XX
 PA (ZAGU/) ZAGURY J.
 PA (ZAGU/) ZAGURY J F.
 XX
 XX Zagury J, Zagury JF;
 PI
 XX WPI; 1994-065602/08.
 DR
 XX New peptide(s) inducing an auto immune response in HIV infected
 PT subjects - also the multimer, proteins contg. them and derived
 PT antibodies, for treating or preventing HIV infection and for
 PT immune suppression
 PT
 XX Claim 1; Page 69; 84pp; French.

XX The sequence SLWDQ is found in the CD4 molecule of human T cells
 CC (residues 60-64) and in the gp120 molecule of HIV-1 (residues 110-
 CC 114 in the LAI strain). The peptide is highly conserved in all
 CC known HIV strains. Peptides containing the SLWDQ sequence elicit a
 CC very strong immune response (both humoral and cellular) in subjects
 CC infected by HIV-1, i.e. an autoimmune reaction. Also, oligopeptides
 CC containing SLWDQ can inhibit T cell activation, probably by competi-
 CC tion with the CD4-CM2 interaction. Antibodies directed against the
 CC peptide or against multimers of the peptide can be therapeutically
 CC used to suppress the immune response in cases of HIV-1 infection.

XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 2 LW 3

RESULT 32
 AAR60079
 ID AAR60079 standard; Protein; 5 AA.
 XX
 AC AAR60079;
 XX
 DT 21-MAR-1995 (first entry)
 XX
 DE TAN-1462A - cyclic ET receptor antagonist.
 XX
 KW Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
 KW antagonist; myocardial infarction; hypertension;
 KW acute renal insufficiency; asthma; cyclic.

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OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 3 /label= alle
FT FT /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT
XX JP061922293-A.
XX
XX 12-JUL-1994.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1994-260512/32.
XX
XX Cyclic penta:peptide(s) - useful as endothelin receptor
XX antagonists for treatment of myocardial infarction, etc.
XX
XX Disclosure; Page 7; 13pp; Japanese.
XX
XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic
XX pentapeptides, useful as endothelin receptor antagonists are given
XX in AAR60079-88. They are useful in the treatment or prophylaxis of
XX hypertension, myocardial infarction, acute renal insufficiency or
XX asthma.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 15; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 LW 5
XX Db 4 LW 5
XX
XX RESULT 34
XX AAR60082
XX ID AAR60082 standard; Protein; 5 AA.
XX
XX AC AAR60082;
XX
XX 21-MAR-1995 (first entry)
XX
XX TAN-1477D - cyclic ET receptor antagonist.
XX
XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
XX antagonist; myocardial infarction; hypertension;
XX acute renal insufficiency; asthma; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Modified-site 3 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX
XX JP061922293-A.
XX
XX 12-JUL-1994.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX 20-JUN-1991; 91JP-0148807.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI; 1994-260512/32.
XX
XX Cyclic penta:peptide(s) - useful as endothelin receptor
XX antagonists for treatment of myocardial infarction, etc.
XX
XX Disclosure; Page 7; 13pp; Japanese.
XX
XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic
XX pentapeptides, useful as endothelin receptor antagonists are given
XX in AAR60079-88. They are useful in the treatment or prophylaxis of
XX hypertension, myocardial infarction, acute renal insufficiency or
XX asthma.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 15; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 LW 5
XX Db 4 LW 5
XX
XX RESULT 33
XX AAR60080
XX ID AAR60080 standard; Protein; 5 AA.
XX
XX AC AAR60080;
XX
XX 21-MAR-1995 (first entry)
XX
XX TAN-1462B - cyclic ET receptor antagonist.
XX
XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
XX antagonist; myocardial infarction; hypertension;
XX acute renal insufficiency; asthma; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Modified-site 3 /note= "D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX
XX JP061922293-A.
XX
XX 12-JUL-1994.
XX

```


CC in AAR60079-88. They are useful in the treatment or prophylaxis of
 CC hypertension, myocardial infarction, acute renal insufficiency or
 CC asthma.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
 ||
 Db 4 LW 5

RESULT 35

AAR60088
 ID AAR60088 standard; Protein; 5 AA.

XX
 AC AAR60088;

XX
 DT 21-MAR-1995 (first entry)

XX TAN-1477K - cyclic ET receptor antagonist.

XX Endothelin; ET; ET-1; ET-2; ET-3; pentapeptide; receptor;
 KW antagonist; myocardial infarction; hypertension;
 KW acute renal insufficiency; asthma; cyclic.

XX Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Modified-site 3

FT /label= alle

FT /note= "D-form residue"

FT Modified-site 5

FT /note= "D-5-methyltryptophan"

FT JP06192293-A.

XX PD 12-JUL-1994.

XX PF 20-JUN-1991; 91JP-0148807.

XX PR 20-JUN-1991; 91JP-0148807.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1994-260512/32.

XX Cyclic penta-peptide(s) - useful as endothelin receptor

XX antagonists for treatment of myocardial infarction, etc.

XX Disclosure; Page 7; 13pp; Japanese.

XX The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic

XX pentapeptides, useful as endothelin receptor antagonists are given

XX in AAR60079-88. They are useful in the treatment or prophylaxis of

XX hypertension, myocardial infarction, acute renal insufficiency or

XX asthma.

XX SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5

||

Db 4 LW 5

RESULT 37

AAR71907

ID AAR71907 standard; peptide; 5 AA.

XX
 AC AAR71907;

XX DT 19-MAY-1995 (first entry)

XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.

XX Chalcogen; ligand; complex; endothelin; non-invasive imaging;

XX technetium; rhenium; in vivo imaging; cyclic.

XX Synthetic.

RESULT 36

AAR62195

ID AAR62195 standard; Protein; 5 AA.

XX
 AC AAR62195;

XX DT 03-MAY-1995 (first entry)

XX CENP-B protein residues 191-195, homologous to SRV-1 protease motif.

XX CENP-B protein; centromere protein; epitope;

XX autoantibody; immunoinfective cluster virus; nuclear protein antigen;

XX systemic lupus erythematosus; SRV-1 viral protease;

XX Homo sapiens.

XX OS WO9420141-A.

XX PN 15-SBP-1994.

XX PD 10-MAR-1994; 94WO-US02631.

XX PF 11-MAR-1993; 93US-0029850.

XX PR (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX PA Douvas A, Ehresmann G, Takehana Y;

XX PI WPI; 1994-302689/37.

XX DR Methods for treating immunoinfective cluster virus infections -

XX PT utilise antibodies or fragments characteristic of auto antibodies

XX PT produced by patients with rheumatic disorders

XX PS Disclosure; Page 71; 106pp; English.

XX CC A comparison of the CENP-B centromere protein sequence with proteins

XX from immunoinfective cluster viruses revealed widespread

XX homologues. The importance of these homologous motifs is that they

XX are epitopes for autoantibodies occurring in high titres in systemic

XX rheumatic disorders. Sera from such patients could be used for

XX treatment of immunoinfective cluster virus infections, e.g. HIV-1,

XX immunoinfective adenoviruses, human lymphotropic retroviruses,

XX rubella virus, CMV and EBV infections.

XX SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5

||

Db 4 LW 5

CC The sequences of ET-1, ET-2 and ET-3 are given in AAR60076-78. Cyclic
 CC pentapeptides, useful as endothelin receptor antagonists are given
 CC in AAR60079-88. They are useful in the treatment or prophylaxis of
 CC hypertension, myocardial infarction, acute renal insufficiency or
 CC asthma.

SQ Sequence 5 AA;

Query Match 65.2%; Score 15; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5

||

Db 4 LW 5

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FH Key Location/Qualifiers
FT Peptide 1..5 /label= cyclic
FT /note= "attached to chalcogen-contg. ligand,
FT see comments"
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 3 /label= alle
FT /note= "D-form residue"
FT Misc-difference 5 /note= "D-form residue"
FT
FT DB4311022-A.
FT
FT PN
FT XX
FT PD 06-OCT-1994.
FT
FT XX 31-MAR-1993; 93DE-4311022.
FT
FT XX 31-MAR-1993; 93DE-4311022.
FT
FT XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
FT
FT XX Dinkelborg L, Hilger C, Kramp W, Schier H;
FT
FT WPI; 1994-311304/39.
FT
FT XX Bis-(N-(mercapto-ethyl- or -propyl) amino:carbonyl:methyl) oxide,
FT sulphide or selenide and derivs. - are ligands for radioactive
FT technetium or thonium for diagnosis and therapy, e.g. for
FT non-invasive in-vivo visualisation of receptors
FT
FT PS Claim 9; Page 14; 15pp; German.
FT
FT XX This peptide is one of 14 endothelin derivatives which are
FT preferred for use in conjugates with novel bis-(N-(mercapto-ethyl-
FT or -propyl) aminocarbonylmethyl) oxide, sulphide or selenide
FT compounds. The chalcogen-containing compounds are ligands which are
FT complexed with a technetium or rhenium radioisotope. The
FT ligand-peptide conjugates are useful for non-invasive, in vivo
FT imaging, e.g. of receptors.
FT
FT XX Sequence 5 AA;
SQ
Query Match 65.2%; Score 15; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LW 5
Db 4 LW 5
RESULT 38
AAR69266
ID AAR69266 standard; peptide; 5 AA.
XX
AC AAR69266;
XX
XX 22-MAY-1995 (first entry)
XX
XX Cyclic pentapeptide having beta-turn and gamma-turn.
XX
XX Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;
XX antiasthmatic; antiinflammatory; antiarthritic;
XX affinity purification; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "D-Glu; and this amino acid is part of a
FT cyclic structure formed by condensation

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FT Modified-site 2 /note= "Ser(Bzl)"
FT Misc-difference 3 /note= "D-Leu"
FT Misc-difference 5 /note= "D-Trp; and this amino acid is condensed
FT onto the N-terminal to form a cyclic
FT peptide"
FT
FT XX EP0606881-A.
FT
FT PN
FT XX 20-JUL-1994.
FT
FT XX 11-JAN-1994; 94EP-0100276.
FT
FT XX 13-JAN-1993; 93JP-0004125.
FT
FT PA (TAKE ) TAKEDA CHEM IND LTD.
FT
FT PI Endo S, Inooka H, Kikuchi T, Wakimasu M;
FT
FT WPI; 1994-226821/28.
FT
FT XX New cyclic penta:peptide(s) having a gamma-turn and a beta-turn -
FT used as NK2 receptor antagonists for treating asthma,
FT inflammation or arthritis
FT
FT PS Claim 10; Page 16; 29pp; English.
FT
FT XX New cyclic pentapeptides are disclosed which have a gamma-turn and a
FT beta-turn and which are of formula Cyclo(-Al-A2-A3-A4-A5-) where the
FT amino acids in positions 1-2-3 form a gamma-turn and the amino acids
FT in positions 3-4-5-1 form a beta-turn in combination with the gamma-
FT turn. Either D-amino acid residues are chosen for A1, A3 and A5 and
FT L-amino acids for A2 and A4; or L-amino acid residues are chosen for
FT A1, A3 and A5 and D-residues for A2 and A5. The peptides are
FT CC antagonists against the NK2 receptor or endothelin receptor. They
FT can be used as antiasthmatic, antiinflammatory or antiarthritic
FT agents or as assay or affinity purification reagents for the
FT receptors.
FT
FT CC The present sequence is a specifically claimed example of the
FT cyclic pentapeptides.
SQ
Query Match 65.2%; Score 15; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 LW 5
Db 4 LW 5
RESULT 39
AAR69267
ID AAR69267 standard; peptide; 5 AA.
XX
AC AAR69267;
XX
XX 22-MAY-1995 (first entry)
XX
XX Cyclic pentapeptide having beta-turn and gamma-turn.
XX
XX Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;
XX antiasthmatic; antiinflammatory; antiarthritic;
XX affinity purification; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1

```

FT	/note= "D-Glu; and this amino acid is part of a
FT	cyclic structure formed by condensation
FT	with the C-terminal amino acid"
FT	
FT	Modified-site 2 /note= "Thr(Bzl) "
FT	Misc-difference 3 /note= "D-Leu"
FT	Misc-difference 5 /note= "D-Trp; and this amino acid is condensed
FT	onto the N-terminal to form a cyclic
FT	peptide"
XX	
PN	EP606881-A.
XX	
PD	20-JUL-1994.
XX	
PX	11-JAN-1994; 94EP-0100276.
XX	
PR	13-JAN-1993; 93JP-0004125.
XX	
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Endo S, Inooka H, Kikuchi T, Wakimasu M;
DR	WPI; 1994-226821/28.
XX	
PT	New cyclic penta;peptide(s) having a gamma-turn and a beta-turn -
PT	used as NK2 receptor antagonists for treating asthma,
PT	inflammation or arthritis
XX	
PS	Claim 11; Page 16; 29pp; English.
XX	
CC	New cyclic pentapeptides are disclosed which have a gamma-turn and a
CC	beta-turn and which are of formula Cyclo(-A1-A2-A3-A4-A5-) where the
CC	amino acids in positions 1-2-3 form a gamma-turn and the amino acids
CC	in positions 3-4-5-1 form a beta-turn in combination with the gamma-
CC	turn. Either D-amino acid residues are chosen for A1, A3 and A5 and
CC	L-amino acids for A2 and A4; or L-amino acid residues are chosen for
CC	A1, A3 and A5 and D-residues for A2 and A5. The peptides are
CC	antagonists against the NK2 receptor or endothelin receptor. They
CC	can be used as antisthmatic, antiinflammatory or antiarthritic
CC	agents or as assay or affinity purification reagents for the
CC	receptors.
CC	The present sequence is a specifically claimed example of the
CC	cyclic pentapeptides.
XX	
XX	Sequence 5 AA;
SQ	
	Query Match 65.2%; Score 15; DB 15; Length 5;
	Best Local Similarity 100.0%; Pred. No. 7.8e+05;
	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	4 LW 5
Dd	4 LW 5
RESULT 40	
AAR69268	
ID	AAR69268 standard; peptide; 5 AA.
XX	
AC	AAR69268;
XX	
DT	22-MAY-1995 (first entry)
XX	
DE	Cyclic pentapeptide having beta-turn and gamma-turn.
XX	
KW	Beta-turn; gamma-turn; NK2; neurokinin; endothelin; receptor;
KW	antasthmatic; antiinflammatory; antiarthritic;
KW	affinity purification; cyclic.
XX	
OS	Synthetic.
XX	

FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-Asp; and this amino acid is part of a
 FT cyclic structure formed by condensation
 FT with the C-terminal amino acid"
 FT
 FT Misc-difference 3 /note= "D-Leu"
 FT Misc-difference 5 /note= "D-Trp; and this amino acid is condensed
 FT onto the N-terminal to form a cyclic
 FT peptide"
 FT
 XX EP606881-A.
 XX
 PD 20-JUL-1994.
 XX
 PF 11-JAN-1994; 94EP-0100276.
 XX
 PR 13-JAN-1993; 93JP-0004125.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Endo S, Inooka H, Kikuchi T, Wakimasu M;
 XX WPI; 1994-226821/28.
 XX
 DR New cyclic penta-peptide(s) having a gamma-turn and a beta-turn -
 XX used as NK2 receptor antagonists for treating asthma,
 PT inflammation or arthritis
 PT
 XX Example 5; Page 15; 29pp; English.
 XX
 CC New cyclic pentapeptides are disclosed which have a gamma-turn and a
 CC beta-turn and which are of formula Cyclo(-A1-A2-A3-A4-A5-) where the
 CC amino acids in positions 1-2-3 form a gamma-turn and the amino acids
 CC in positions 3-4-5-1 form a beta-turn in combination with the gamma-
 CC turn. Either D-amino acid residues are chosen for A1, A3 and A5 and
 CC L-amino acids for A2 and A4; or L-amino acid residues are chosen for
 CC A1, A3 and A5 and D-residues for A2 and A5. The peptides are
 CC antagonists against the NK2 receptor or endothelin receptor. They
 CC can be used as antiasthmatic, antiinflammatory or antiarthritic
 CC agents or as assay or affinity purification reagents for the
 CC receptors.
 CC The present sequence is a specific example of the cyclic
 CC pentapeptides.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 4 LW 5
 RESULT 42
 AAR65742
 ID AAR65742 standard; peptide; 5 AA.
 XX
 AC AAR65742;
 XX
 XX 09-JUN-1995 (first entry)
 XX
 XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.
 DE Chalcogen; ligand; complex; endothelin; non-invasive imaging;
 KW technetium; rhenium; in vivo imaging; atherosclerotic plaque;
 KW bifunctional chalcogen-interrupted chelate former; cyclic.
 XX
 OS Synthetic.
 XX

FH Key Location/Qualifiers
 FT Peptide 1.5
 FT /label= cyclic
 FT /note= "attached to chalcogen-contg. ligand,
 FT see comments"
 FT
 FT Misc-difference 1 /note= "D-form residue"
 FT Modified-site 3 /label= alle
 FT /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 1 /note= "the amino group of D-Glu forms a peptide
 FT linkage with the carboxy group of D-Trp"
 FT Modified-site 5 /note= "the amino group of D-Glu forms a peptide
 FT linkage with the carboxy group of D-Trp"
 FT
 XX DE4311023-A.
 XX
 PD 06-OCT-1994.
 XX
 XX 31-MAR-1993; 93DE-4311023.
 PF
 XX 31-MAR-1993; 93DE-4311023.
 PR
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA
 XX Dinkelborg L, Hilger C, Kramp W, Schier H;
 PI WPI; 1994-311305/39.
 XX
 DR Bifunctional chalcogen-atom interrupted chelate formers - for
 XX radioactive isotopes, their prodn. and use in diagnostics and
 PT therapy, e.g. for non-invasive in-vivo representation of
 PT receptors
 PT
 XX Claim 9; Page 11; 13pp; German.
 XX
 XX This peptide is one of 14 endothelin derivatives which are
 CC preferred for use in conjugates with novel, bifunctional chalcogen-
 CC interrupted chelate forming compounds. The chalcogen-containing
 CC compounds are ligands which are complexed with a technetium or
 CC rhenium radioisotope. The ligand-peptide conjugates are useful
 CC for non-invasive, in vivo imaging, e.g. of receptors or of
 CC atherosclerotic plaques.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 4 LW 5
 RESULT 43
 AAR65728
 ID AAR65728 standard; peptide; 5 AA.
 XX
 AC AAR65728;
 XX
 XX 02-JUN-1995 (first entry)
 XX
 XX Endothelin cyclic peptide conjugated to chalcogen-contg. ligand.
 DE Chalcogen; ligand; complex; endothelin; non-invasive imaging;
 KW technetium; rhenium; in vivo imaging; atherosclerotic plaque;
 KW bifunctional chalcogen-interrupted chelate former; cyclic.
 XX
 OS Synthetic.
 XX

OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..5
 FT /label= cyclic
 FT /note= "attached to chalcogen-contg. ligand,
 FT see comments"
 FT Misc-difference 1 /note= "D-form residue"
 FT Modified-site 3 /label= aile
 FT /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT DE4310999-A.
 PN 06-OCT-1994.
 XX 31-MAR-1993; 93DE-4310999.
 XX 31-MAR-1993; 93DE-4310999.
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA Dinkelborg L, Hilger C, Kramp W, Schier H;
 FI WPI; 1994-311297/39.
 DR
 XX Bifunctional, chalcogen-interrupted chelate former for
 FT radioisotopes - used in diagnostics and therapy, e.g. for
 FT non-invasive in-vivo representation of receptors
 XX Claim 9; Page 12; 13pp; German.
 XX This peptide is one of 14 endothelin derivatives which are
 CC preferred for use in conjugates with novel, bifunctional chalcogen-
 CC interrupted chelate forming compounds. The chalcogen-containing
 CC compounds are ligands which are complexed with a technetium or
 CC rhodium radioisotope. The ligand-peptide conjugates are useful
 CC for non-invasive, in vivo imaging, e.g. of receptors or of
 CC atherosclerotic plaques.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 4 LW 5
 RESULT 44
 AAR63183
 ID AAR63183 standard; peptide; 5 AA.
 XX
 AC AAR63183;
 XX 16-JUN-1995 (first entry)
 DT Cyclic peptide ligand #2 for radiopharmaceutical agent.
 XX Peptide; ligand; radioactive; peptide complex; imaging; receptor;
 KW steroid; hormone; atherosclerotic plaque; targeting; endothelin;
 KW analogue; derivative; antagonist.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "Forms peptide linkage with DTrp5"
 FT

FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 3 /note= "alloDile"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 5 /note= "Forms peptide linkage with DGIu1"
 XX WO9422491-A.
 PN 13-OCT-1994.
 XX 29-MAR-1994; 94WO-DE00369.
 XX 31-MAR-1993; 93DE-4311021.
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA Dinkelborg L, Erber S, Noll B, Rohlf G, Schulze P;
 FI WPI; 1994-332837/41.
 DR
 XX New radio-pharmaceutical agents deriv. from peptide chelating
 FT ligands - also the new ligands and complexes with tissue
 FT targeting peptide(s), useful for imaging and treatment of e.g.
 PT atherosclerosis or steroid dependent cancer
 XX Claim 14; Page 66; 81pp; German.
 XX The sequences given in AAR73170-83 represent peptide ligands which are
 CC used with the radioactive peptide complex of the invention. The
 CC complexes may be used to image receptors, specifically of steroid
 CC hormones, receptor contg. tissue and/or atherosclerotic plaque.
 CC These peptides allow the complex to be targeted to a specific
 CC tissue. These peptides are pref. derived from endothelin, and
 CC represent analogues, derivatives or antagonists.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 4 LW 5
 RESULT 45
 AAR64367
 ID AAR64367 standard; Peptide; 5 AA.
 XX
 AC AAR64367;
 XX 25-AUG-1995 (first entry)
 DT DP-178 homologue 36 derived from HIV-1 has antiviral activity.
 XX
 DE antitiral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
 KW human immunodeficiency virus; transmembrane protein; gp41;
 KW alpha helix; leucine zipper; DP-185.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "optionally has an amino, acetyl,
 FT 9-fluorenylmethoxy-carbonyl, hydrophobic or
 FT macromolecular carrier gp. attached"
 FT Modified-site 5 /note= "optionally has a carboxyl, amido, hydrophobic
 FT or macromolecular carrier gp. attached"
 FT

XX WO9428920-A.
 XX 22-DEC-1994.
 XX 07-JUN-1994; 94WO-US05739.
 XX 07-JUN-1993; 93US-0073028.
 XX (UYDU-) UNIV DUKE.
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TU;
 PI Petteway SR, Wild CT;
 XX WPI; 1995-036105/05.
 XX Computer search generated synthetic peptides - are inhibitors of
 PT HIV transmission
 XX Claim 11; Page 133; 182pp; English.
 XX AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been
 CC truncated at the amino terminus. DP-178 corresponds to amino acids
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It
 CC forms a putative alpha helix at the C-terminal end of the gp41
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids
 CC 558-595) which contains a leucine zipper motif. The peptides complex
 CC via non-covalent protein-protein interactions, and possess anti-viral
 CC activity. The peptide derivs. were identified by a computer assisted
 CC peptide sequence search. The peptides inhibit transmission to
 CC uninfected cells, and can also be used as type and/or subtype
 CC specific diagnostic tools.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 1 LW 2
 RESULT 46
 AAR59459
 ID AAR59459 standard; peptide; 5 AA.
 AC AAR59459;
 XX 01-SEP-1995 (first entry)
 XX Melanin pigmentation inhibiting cyclic pentapeptide.
 XX Melanin pigmentation inhibition; skin whitening cosmetic;
 KW cyclic pentapeptide; sunburn fleck formation treatment.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "forms peptide bond with Xaa at position 5"
 FT /note= "D or L form residues"
 FT Misc-difference 2 /label= Glu, Asp
 FT Misc-difference 3 /note= "D or L form residues"
 FT Misc-difference 4 /label= Ala, Pro, Hyp
 FT Misc-difference 5 /note= "D or L form residues"
 FT /label= Val, Asp

FT Modified-site 5 /note= "D or L form residues"
 FT /note= "forms peptide bond with Leu at position 1"
 XX JP06321755-A.
 XX 22-NOV-1994.
 XX 11-MAY-1993; 93JP-0109456.
 XX 11-MAY-1993; 93JP-0109456.
 XX (KAOS) KAO CORP.
 XX WPI; 1995-041168/06.
 XX Skin whitening cosmetic contg. cyclic penta-peptide - e.g.
 PT cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin
 PT pigmentation
 XX Claim 1; Page 2; 7pp; Japanese.
 XX AAR59459-R59461 are cyclic pentapeptides which inhibit melanin
 CC pigmentation. As part of a skin whitening cosmetic they can be
 CC used for the prevention of fleck formation after sunburn.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 1 LW 2
 RESULT 47
 AAR59460
 ID AAR59460 standard; peptide; 5 AA.
 AC AAR59460;
 XX 01-SEP-1995 (first entry)
 XX Melanin pigmentation inhibiting cyclic pentapeptide.
 XX Melanin pigmentation inhibition; skin whitening cosmetic;
 KW cyclic pentapeptide; sunburn fleck formation treatment.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "forms peptide bond with Val at position 5"
 FT /note= "D or L form residues"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 5 /note= "forms peptide bond with Leu at position 1"
 XX JP06321755-A.
 XX 22-NOV-1994.
 XX 11-MAY-1993; 93JP-0109456.
 XX 11-MAY-1993; 93JP-0109456.
 XX (KAOS) KAO CORP.

XX WPI; 1995-041168/06.
 XX Skin whitening cosmetic contg. cyclic penta:peptide - e.g.
 PT cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin
 PT pigmentation
 XX
 PS Example 1; Page 3; 7pp; Japanese.
 XX
 CC AAR59459-R59461 are cyclic pentapeptides which inhibit melanin
 CC pigmentation. As part of a skin whitening cosmetic they can be
 CC used for the prevention of fleck formation after sunburn.
 XX

SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 1 LW 2

RESULT 48
 AAR59461
 ID AAR59461 standard; peptide; 5 AA.
 XX
 AC AAR59461;
 XX
 DT 01-SEP-1995 (first entry)
 XX
 DE Melanin pigmentation inhibiting cyclic pentapeptide.
 XX
 DE Melanin pigmentation inhibition; skin whitening cosmetic;
 KW cyclic peptide; sunburn fleck formation treatment.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "forms peptide bond with Asp at position 5"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 3 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Modified-site 5 /note= "forms peptide bond with Leu at position 1"
 FT
 PN JP06321755-A.
 XX
 PD 22-NOV-1994.
 XX
 PF 11-MAY-1993; 93JP-0109456.
 XX
 PR 11-MAY-1993; 93JP-0109456.
 XX
 PA (KAOS) KAO CORP.
 XX
 DR WPI; 1995-041168/06.
 XX
 XX Skin whitening cosmetic contg. cyclic penta:peptide - e.g.
 PT cyclo(L-Leu-D-Trp-D-Glu-L-Ala-D-Val), for inhibiting melanin
 PT pigmentation
 XX
 PS Example 1; Page 3; 7pp; Japanese.
 XX
 CC AAR59459-R59461 are cyclic pentapeptides which inhibit melanin
 CC pigmentation. As part of a skin whitening cosmetic they can be
 CC used for the prevention of fleck formation after sunburn.
 XX

SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 1 LW 2

RESULT 49
 AAR69429
 ID AAR69429 standard; peptide; 5 AA.
 XX
 AC AAR69429;
 XX
 DT 18-JUL-1995 (first entry)
 XX
 DE Cyclic endothelin receptor peptide for treating organ hypofunction.
 XX
 KW Endothelin receptor antagonist; organ hypofunction; liver; surgery;
 KW transplant; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-Asp, which is part of a cyclic peptide
 FT Modified-site 2 /note= "D-Trp(5)"
 FT /label= OTHER
 FT /note= "alpha-amino acid with conformationally
 FT restricted 4-16C side chain, preferably
 FT 1,2,3,4-tetrahydro-2-carboline-3-carboxylic
 FT acid"
 FT Misc-difference 3 /note= "D-Val"
 FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide
 FT /note= "D-Trp(1)"
 FT
 PN EP626174-A.
 XX
 PD 30-NOV-1994.
 XX
 PF 20-APR-1994; 94EP-0106093.
 XX
 PR 21-APR-1993; 93JP-0094332.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Kitada C, Wakimasu M, Watanabe T;
 PI WPI; 1995-000740/01.
 XX
 DR Use of endothelin receptor antagonists - for prophylaxis or
 PT treatment of organ hypofunction, partic. caused by surgery on or
 PT transplant of the organ
 XX
 PS Claim 34; Page 106; 107pp; English.
 XX
 CC The invention relates to the new use of known endothelin receptor
 CC antagonists for prophylaxis and/or therapy of hypofunction of organs
 CC (particularly the liver) which occurs following their surgery or
 CC transplant. The present sequence is a specific example of a suitable
 CC antagonist listed in the Claims.
 XX

SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
DB 4 LW 5

RESULT 50

AAR69430
ID AAR69430 standard; peptide; 5 AA.

XX AC AAR69430;
XX 18-JUL-1995 (first entry)

XX Cyclic endothelin receptor peptide for treating organ hypofunction.
DE Endothelin receptor antagonist; organ hypofunction; liver; surgery;
KW transplant; cyclic.
XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-Ser, which is part of a cyclic peptide
formed by condensation with D-Trp(5)"

FT Modified-site 2 /label= OTHER
FT /note= "alpha-amino acid with conformationally
restricted side chain"

FT Misc-difference 3 /note= "D-Val"

FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide
formed by condensation with D-Ser(1)"

XX EP626174-A.

XX 30-NOV-1994.

XX 20-APR-1994; 94EP-0106093.

XX 21-APR-1993; 93JP-0094332.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kitada C, Wakimasu M, Watanabe T;

XX WPI; 1995-000740/01.

XX Use of endothelin receptor antagonists - for prophylaxis or
treatment of organ hypofunction, partic. caused by surgery on or
transplant of the organ

XX Claim 34; Page 106; 107pp; English.

XX The invention relates to the new use of known endothelin receptor
antagonists for prophylaxis and/or therapy of hypofunction of organs
(particularly the liver) which occurs following their surgery or
transplant. The present sequence is a specific example of a suitable
antagonist listed in the Claims.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
DB 4 LW 5

RESULT 51

AAR69414
ID AAR69414 standard; peptide; 5 AA.

XX AC AAR69414;
XX 18-JUL-1995 (first entry)

XX Cyclic endothelin receptor peptide for treating organ hypofunction.
DE Endothelin receptor antagonist; organ hypofunction; liver; surgery;
KW transplant; cyclic.
XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-Cys(03S), which is part of a cyclic peptide
formed by condensation with D-Trp(5)"

FT Misc-difference 3 /note= "D-Val"

FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide
formed by condensation with D-Cys(1)"

XX EP626174-A.

XX 30-NOV-1994.

XX 20-APR-1994; 94EP-0106093.

XX 21-APR-1993; 93JP-0094332.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kitada C, Wakimasu M, Watanabe T;

XX WPI; 1995-000740/01.

XX Use of endothelin receptor antagonists - for prophylaxis or
treatment of organ hypofunction, partic. caused by surgery on or
transplant of the organ

XX Claim 12; Page 86; 107pp; English.

XX The invention relates to the new use of known endothelin receptor
antagonists for prophylaxis and/or therapy of hypofunction of organs
(particularly the liver) which occurs following their surgery or
transplant. The present sequence is a specific example of a suitable
antagonist listed in the Claims.

XX Sequence 5 AA;

Query Match 65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LW 5
DB 4 LW 5

RESULT 52

AAR69415
ID AAR69415 standard; peptide; 5 AA.

XX AC AAR69415;
XX 18-JUL-1995 (first entry)

XX Cyclic endothelin receptor peptide for treating organ hypofunction.
DE Endothelin receptor antagonist; organ hypofunction; liver; surgery;
KW transplant; cyclic.


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XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "D-Thg(2) or D-Cpg, where Thg(2) is 2-(2-
FT thienyl)glycine and Cpg is 2-cyclopentyl-
FT glycine"
FT
FT Misc-difference 3 /label= OTHER
FT
FT Misc-difference 5 /note= "D-Trp, which is part of a cyclic peptide
FT formed by condensation with D-Asp(1)"
FT
XX EP626174-A.
XX
XX 30-NOV-1994.
XX
XX 20-APR-1994; 94EP-0106093.
XX
XX 21-APR-1993; 93JP-0094332.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kitada C, Wakimasu M, Watanabe T;
XX
XX WPI; 1995-000740/01.
XX
XX Use of endothelin receptor antagonists - for prophylaxis or
XX treatment of organ hypofunction, partic. caused by surgery on or
XX transplant of the organ
XX
XX Claim 12; Page 86; 107pp; English.
XX
XX The invention relates to the new use of known endothelin receptor
XX antagonists for prophylaxis and/or therapy of hypofunction of organs
XX (particularly the liver) which occurs following their surgery or
XX transplant. The present sequence is a specific example of a suitable
XX antagonist listed in the Claims.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 16; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 LW 5
XX ||
XX Db 4 LW 5
XX
XX RESULT 53
XX AAR69413
XX ID AAR69413 standard; peptide; 5 AA.
XX
XX AC AAR69413;
XX
XX DT 18-JUL-1995 (first entry)
XX
XX DE Cyclic endothelin receptor peptide for treating organ hypofunction.
XX
XX KW Endothelin receptor antagonist; organ hypofunction; liver; surgery;
XX transplant; cyclic.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-Asp, which is part of a cyclic peptide
XX formed by condensation with D-Trp(5)"
XX
XX FT Misc-difference 3

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FT Misc-difference 5 /note= "D-Val"
FT
FT FT /note= "D-Trp, which is part of a cyclic peptide
FT formed by condensation with D-Asp(1)"
XX
XX EP626174-A.
XX
XX 30-NOV-1994.
XX
XX 20-APR-1994; 94EP-0106093.
XX
XX 21-APR-1993; 93JP-0094332.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kitada C, Wakimasu M, Watanabe T;
XX
XX WPI; 1995-000740/01.
XX
XX Use of endothelin receptor antagonists - for prophylaxis or
XX treatment of organ hypofunction, partic. caused by surgery on or
XX transplant of the organ
XX
XX Claim 12; Page 86; 107pp; English.
XX
XX The invention relates to the new use of known endothelin receptor
XX antagonists for prophylaxis and/or therapy of hypofunction of organs
XX (particularly the liver) which occurs following their surgery or
XX transplant. The present sequence is a specific example of a suitable
XX antagonist listed in the Claims.
XX
XX Sequence 5 AA;
XX
XX Query Match 65.2%; Score 15; DB 16; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 LW 5
XX ||
XX Db 4 LW 5
XX
XX RESULT 54
XX AAR69392
XX ID AAR69392 standard; peptide; 5 AA.
XX
XX AC AAR69392;
XX
XX DT 16-JUL-1995 (first entry)
XX
XX DE Endothelin antagonist peptide for treating organ hypofunction.
XX
XX KW Endothelin receptor antagonist; organ hypofunction; liver; surgery;
XX transplant; cyclic.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "hexamethyleneimino-CO-Leu"
XX
XX FT Misc-difference 2 /label= D-Trp
XX
XX FT Misc-difference 3 /note= "D-Ala"
XX
XX FT Modified-site 4 /label= bAla
XX
XX FT Modified-site 5 /note= "Tyr-NH-Ind-OH, where Ind is
XX 1-carboxyindane-2-yl"
XX
XX EP626174-A.
XX
XX 30-NOV-1994.
XX

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XX PF 20-APR-1994; 94EP-0106093.
 XX PR 21-APR-1993; 93JP-0094332.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Kitada C, Wakimasu M, Watanabe T;
 XX WPI; 1995-000740/01.
 XX Use of endothelin receptor antagonists - for prophylaxis or
 PT treatment of organ hypofunction, partic. caused by surgery on or
 PT transplant of the organ
 XX Claim 7; Page 83; 107pp; English.
 XX The invention relates to the new use of known endothelin receptor
 CC antagonists for prophylaxis and/or therapy of hypofunction of organs
 CC (particularly the liver) which occurs following their surgery or
 CC transplant. The present sequence is a specific example of a suitable
 CC antagonist listed in the Claims.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 1 LW 2

RESULT 55
 AAR86453
 ID AAR86453 standard; peptide; 5 AA.
 XX AC AAR86453;
 XX DT 05-FEB-1996 (first entry)
 XX DE Endothelin sequence for use as conjugate with Cys-free peptide.
 XX diagnostic imaging; atherosclerotic plaque; tumour; inflammation;
 KW conjugate; radiotherapy; cysteine-free; metal-binding; endothelin;
 KW cyclic.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue; and this amino acid forms
 FT part of a cyclic structure obtained by
 FT condensation of D-Trp(5) onto the alpha-NH2"
 FT Misc-difference 3 /label= alle
 FT /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue; and this amino acid forms
 FT part of a cyclic structure formed by
 FT condensation of the COOH onto the NH2 group
 FT of D-Glu(1)"
 XX DB4337599-A1.
 XX 04-MAY-1995.
 XX 01-NOV-1993; 93DE-4337599.
 XX 01-NOV-1993; 93DE-4337599.
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.

XX Conrad J, Dinkelborg L, Erber S, Frommel C, Hohne W;
 PI Kramp W, Kuttner G, Malin R, Schier HM, Schneider-Mergener J;
 PI Steinbrecher R, Froemmel C, Hoehne W, Kuettnner G, Schier H;
 XX WPI; 1995-171400/23.
 XX New cysteine-free peptide(s) and their metal ion complexes - opt.
 PT conjugated to targeting agent, useful for in vivo imaging of
 PT tumours, atherosclerotic plaque etc. and for radiotherapy
 XX Claim 13; Page 20; 25pp; German.
 XX New peptides of formula R1-X-R2 are provided, together with their
 CC conjugates with peptides, proteins, biomolecules and macromolecules,
 CC their complexes with metal ions and their water-soluble salts; where
 CC X is a chain of up to 20 alpha, beta, and/or gamma amino acid residues,
 CC including at least one Met, Arg, Lys or Asn but no Cys; R1 is H or a
 CC hydrocarbyl or acyl group, or a bond to a conjugate; and R2 is OH,
 CC hydrocarbyl or an optionally substituted amine group (forming an
 CC amide), or a bond to a conjugate. The peptides are useful when complexed
 CC to a metal (e.g. 99m-Tc) for in-vivo diagnostic imaging and therapy of
 CC tumours, organs and foci of inflammation. Conjugates of the peptides can
 CC be targeted to specific tissues. A particular application is imaging of
 CC atherosclerotic plaque. Metal is bound with good in-vivo stability;
 CC unbound material is rapidly cleared; and there is no allergic reaction.
 CC Since the peptides are free of Cys, they can be prepared simply and
 CC rapidly and can be presented in the form of a kit for radio-
 CC pharmaceutical production. Specific examples of the peptides are
 CC given in AAR86424 - AAR86439.
 CC The present sequence is a specific example of an endothelin peptide
 CC which can be used as a conjugate with the new peptides.
 XX SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 Db 4 LW 5

RESULT 56
 AAW17809
 ID AAW17809 standard; peptide; 5 AA.
 XX AC AAW17809;
 XX DT 07-JUL-1997 (first entry)
 XX Cyclic pentapeptide #25 used in LH-RH receptor antagonist.
 DE Lutetising hormone releasing hormone receptor; LH-RH; antagonist;
 DE sex-hormone; human; veterinary medicine; cancer; prostate; uterus;
 KW breast; pituitary; prostatic; endometriosis; hysteromyoma;
 KW precocious puberty; amenorrhoea; premenstrual syndrome; cyclic;
 KW multilocular ovarian syndrome; comedo; pregnancy; contraception;
 KW ovulation; menstrual cycle; oestrus; meat quality; growth; spawning;
 KW fish; testosterone; superagonist; leuprorelin acetate.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Joined via a peptide linkage to Trp5"
 FT Modified-site 2 /note= "N-pToluenesulphonylarginine, D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT Modified-site 5 /note= "Joined via a peptide linkage to Phe1"
 XX Synthetic.

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XX PN WO9634012-A1.
XX PD 31-OCT-1996.
XX PF 25-APR-1996; 96WO-JP01140.
XX PR 09-MAY-1995; 95JP-0110933.
XX PR 28-APR-1995; 95JP-0106775.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Furuya S, Kato K, Kitada C;
XX DR WPI; 1996-497569/49.
XX PT Cyclic penta;peptide(s), some new, as LH-RH receptor antagonists -
XX PT used to treat or prevent sex hormone dependent disorders, e.g.
XX PT cancer, also for control of pregnancy and menstruation and to
XX PT improve meat quality in animals
XX PS Example 45; Page 173; 198pp; English.
XX CC This peptide represents a cyclic peptide which is included in the
XX CC luteinising hormone releasing hormone (LH-RH) receptor antagonist
XX CC composition of the invention. Peptides such as this are used to
XX CC prevent or treat sex-hormone dependent disorders in human or veterinary
XX CC medicine, esp. cancers (of the prostate, uterus, breast or pituitary),
XX CC prostatically, endometriosis, hysteromyoma or precocious puberty, but
XX CC also amenorrhoea, premenstrual syndrome, multilocular ovarian syndrome,
XX CC conedo, etc.; also to control pregnancy (contraction for men or women,
XX CC also to induce ovulation) and the menstrual cycle. They are also used
XX CC to control oestrus in animals, to improve meat quality and control
XX CC growth, and to promote spawning in fish. They may also inhibit the
XX CC transient increase in testosterone blood levels caused by admin. of
XX CC superagonists such as leuprolerin acetate.
XX SQ Sequence 5 AA;
    Query Match 65.2%; Score 15; DB 17; Length 5;
    Best Local Similarity 40.0%; Pred. No. 7.8e+05;
    Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 FXXLW 5
Db 1 FRFFW 5
RESULT 57
AAR86236
ID AAR86236 standard; peptide; 5 AA.
XX AC
XX AC AAR86236;
XX DT 27-JUN-1996 (first entry)
XX DE Anti-ELAM-1 binding peptide #213.
XX KW Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin;
XX KW receptor; leukocyte; vascular wall; endothelium; extravasation;
XX KW inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Ac-Leu"
XX FT Modified-site 5 /note= "amidated C-terminus"
XX FT
XX PN WO9531210-A1.
XX PD 23-NOV-1995.
XX PF 11-MAY-1995; 95WO-US06315.
XX PR 11-MAY-1994; 94US-0241054.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PI Barrett RW, Cwirila SE, Dower WJ, Koller KJ, Lee J;
XX PI Martens CL, Ruhland-fritsch B;
XX DR WPI; 1996-010687/01.
XX PT New peptide(s) that bind to endothelial leukocyte adhesion molecule
XX PT 1 - useful for treating inflammation and other E-selectin mediated
XX PT diseases
XX PS Claim 3; Page 73; 85pp; English.
XX CC Peptides AAR86024-R86236 are examples of peptides and their mimetics
XX CC that bind to endothelial leukocyte adhesion molecule (ELAM)-1. This
XX CC molecule is a member of the selectin family of receptors and is involved
XX CC in binding of leukocytes to the vascular endothelial wall prior to
XX CC extravasation of the leukocyte, e.g. to a site of inflammation.
XX CC The peptides bind pref. to E-selectin but may also bind L- or
XX CC P-selectin, and can be used to treat conditions mediated by E-selectin,
XX CC e.g. inflammatory conditions. The peptides have strong affinity for the
XX CC selectin receptors and inhibit the binding of the sialyl Lewis (SLe-x)
XX CC part of cell surface glycoproteins to E-selectin. The peptide are
XX CC small, generally less than 2 KD, have an IC50 of up to 100 micromole
XX CC against binding of HL60 cells to ELAM-1, have one or more peptide
XX CC linkages replaced by CH2OC(O)NR, phosphonate, CH2SO2NR, CH2NR, CON(R6),
XX CC or NHC(=O)NH linkages where R = H or a lower alkyl and R6 = a lower alkyl.
XX CC The peptides may also have substituted N- and C-termini e.g.
XX CC succinimido, N-benzoyloxycarbonyl or N-lower alkyl cpds.
XX SQ Sequence 5 AA;
    Query Match 65.2%; Score 15; DB 17; Length 5;
    Best Local Similarity 100.0%; Pred. No. 7.8e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
Db 1 LW 2
RESULT 58
AAW33328
ID AAW33328 standard; peptide; 5 AA.
XX AC
XX AC AAW33328;
XX DT 05-FEB-1998 (first entry)
XX DE Targeting conjugate for bis-nicotinamide bifunctional chelator.
XX KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;
XX KW rhenium; conjugate; endothelin; angiotensin; targeting agent;
XX KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
XX KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
XX KW delivery; cyclic.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Misc-difference 3 /note= "allo-D-form residue"
XX FT Misc-difference 5 /note= "D-form residue"
XX FT

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[illegible]

PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 XX WPI; 1997-193894/18.
 XX Bifunctional sulphonamide type ligands for radioactive technetium or
 PT rhenium - and their chelates and conjugates, useful for imaging
 PT carcinoma or atherosclerosis
 XX Claim 9; Page 12; 12pp; German.
 XX Novel bifunctional sulphonamide type ligands for radioactive
 CC technetium and rhenium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.
 XX Sequence 5 AA;
 SQ Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 4 LW 5
 ||
 RESULT 61
 AAW11213
 ID AAW11213 standard; peptide; 5 AA.
 XX AAW11213;
 XX 26-JAN-1998 (first entry)
 DT Targetting conjugate for bifunctional sulphonamide type ligand.
 DE Bifunctional sulphonamide; ligand; radioactive; technetium;
 KW rhenium; conjugate; endothelin; angiotensin; targeting agent;
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
 KW delivery; cyclic.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 3 /note= "allo D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT DE19536780-A1.
 XX 27-MAR-1997.
 XX 21-SEP-1995; 95DE-1036780.
 XX 21-SEP-1995; 95DE-1036780.
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 XX Raduechel B;
 XX WPI; 1997-193892/18.
 XX Bifunctional sulphonamide type ligands for radioactive technetium
 PT and rhenium - and their chelates and conjugates with targeting
 PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.
 XX Claim 11; Page 19; 19pp; German.

XX Bifunctional sulphonamide type ligands for radioactive technetium
 PT and rhenium - and their chelates and conjugates with targeting
 PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.
 XX Claim 11; Page 19; 19pp; German.
 XX Novel bifunctional sulphonamide type ligands for radioactive
 CC technetium and rhenium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.
 XX Sequence 5 AA;
 SQ Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 ||
 Db 4 LW 5
 ||
 RESULT 62
 AAW11212
 ID AAW11212 standard; peptide; 5 AA.
 XX AAW11212;
 XX 26-JAN-1998 (first entry)
 DT Targetting conjugate for bifunctional sulphonamide type ligand.
 DE Bifunctional sulphonamide; ligand; radioactive; technetium;
 KW rhenium; conjugate; endothelin; angiotensin; targeting agent;
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
 KW delivery; cyclic.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 4 /note= "D-form residue"
 FT DE19536780-A1.
 XX 27-MAR-1997.
 XX 21-SEP-1995; 95DE-1036780.
 XX 21-SEP-1995; 95DE-1036780.
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 XX WPI; 1997-193892/18.
 XX Bifunctional sulphonamide type ligands for radioactive technetium
 PT and rhenium - and their chelates and conjugates with targeting
 PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.
 XX Claim 11; Page 19; 19pp; German.

XX Novel bifunctional sulphonamide type ligands for radioactive
 CC technetium and rhodium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.

XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 4 LW 5

RESULT 63
 AAW14986
 ID AAW14986 standard; peptide; 5 AA.
 AC AAW14986;
 XX
 DT 28-NOV-1997 (first entry)
 DE
 XX Conjugating cyclic peptide for radio-therapeutic/diagnostic agent.
 XX Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;
 KW radiodiagnostic; radiotherapeutic; diagnosis; tumour; ischaemia;
 KW atherosclerosis; vascular disorder; ischemia; circular; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 3
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 XX
 PN WO9710852-A2.
 XX
 PD 27-MAR-1997.
 XX
 PF 19-SEP-1996; 96WO-DR01821.
 XX
 PR 21-SEP-1995; 95DE-4036781.
 XX
 PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 XX
 DR WPI; 1997-202627/18.
 XX
 PT New sulphide-sulphonamide bi:functional chelating agents - forming
 PT new, stable technetium or rhodium complexes and conjugates useful as
 PT radiodiagnostic and radio-therapeutic agents
 XX
 PS Claim 13; Page 45; 50pp; German.
 XX
 CC XSNS-type bifunctional sulphide containing sulphonamide chelating
 CC agents and their technetium or rhodium complexes, can form
 CC covalently bonded conjugates with substances selectively enriched
 CC in diseased tissue, e.g. the present peptide. The substance is an
 CC endothelin or angiotensin peptide, or a partial sequence, analogue,
 CC derivative or antagonist, or a chemotactic peptide.
 CC The conjugates are radiodiagnostic or radiotherapeutic agents,
 CC useful in the diagnosis of tumours, ischaemia or atherosclerotic

CC vascular disorders.
 XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 4 LW 5

RESULT 64
 AAW22915
 ID AAW22915 standard; peptide; 5 AA.
 AC AAW22915;
 XX
 DT 02-OCT-1997 (first entry)
 DE
 XX Low density lipoprotein binding peptide.
 XX Low density; lipoprotein; LDL; binding; absorbent; removal;
 KW body fluid; reagent.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 5 /note= "amidated"
 XX
 PN WO9700889-A1.
 XX
 PD 09-JAN-1997.
 XX
 PF 21-JUN-1996; 96WO-JP01734.
 XX
 PR 21-JUN-1995; 95JP-0176904.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PA (ASAH) ASAH MEDICAL CO LTD.
 XX
 PI Aritomi M, Hatanaka Y;
 XX
 DR WPI; 1997-087320/08.
 XX
 PT Peptide binding to low density lipoprotein - useful in removing LDL
 PT from body fluids and as carrier peptide(s) for drugs
 XX
 PS Example 11; Page 50; 61pp; Japanese.
 XX
 CC The present low density lipoprotein (LDL) binding peptide can be
 CC used as an absorbent to remove LDL from body fluids, or as a
 CC LDL binding reagent. The peptide can be prepared easily and at low
 CC cost, and has excellent stability and preservability. It
 CC specifically binds LDL, and does not cause bradykinin production,
 CC white blood cell activation or blood agglutination.

XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 4 LW 5

RESULT 65
 AAW22920
 ID AAW22920 standard; peptide; 5 AA.

[illegible]

XX PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX DR WPI; 1998-609901/51.
 XX DR N-PSDB; AAX75757.
 XX PT Diagnosing disease by detecting frameshift mutations in RNA or
 XX PT corresponding protein mutations - used to diagnose cancer and
 XX PT neurological diseases, particularly Alzheimer's disease, and also
 XX PT for treatment and prevention with specific ribozymes or wild-type
 XX PT RNA
 XX PS Disclosure; Figure 6; 258pp; English.
 XX CC This invention describes a novel method for the diagnosis of a disease
 XX CC caused by, or associated with, an RNA molecule that has a frameshift
 XX CC mutation. The method is used to diagnose age-related diseases, especially
 XX CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 XX CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 XX CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 XX CC and many others listed) or susceptibility to these disorders. The method
 XX CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 XX CC at an early stage. It is based on the observation that disease may be
 XX CC caused by mutations in RNA rather than DNA. The invention describes the
 XX CC use of neuronal system RNA molecules, specifically proteins including
 XX CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 XX CC protein Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 XX CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 XX CC neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic
 XX CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 XX CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 XX CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX SQ Sequence 5 AA;
 XX Query Match 65.2%; Score 15; DB 19; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 1 LW 2
 RESULT 68
 ID AAW65861
 AC AAW65861;
 XX 19-OCT-1998 (first entry)
 DE Endothelin receptor binding peptide part of conjugate.
 XX endothelin receptor; antagonist; atherosclerosis; radionuclide;
 KW tyrosine kinase blocker; chemotherapy; antibody; conjugate; cyclic.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "D-Glu is condensed onto D-Trp at position 5
 FT to form a cyclic peptide"
 FT Modified-site 3 /label= alle
 FT /note= "D-form allo-isoleucine"
 FT Modified-site 5
 FT /note= "D-Trp is condensed onto D-Glu at position 1
 FT to form a cyclic peptide"
 XX DE19652374-A1.
 XX 10-JUN-1998.

XX PF 04-DEC-1996; 96DE-1052374.
 XX PR 04-DEC-1996; 96DE-1052374.
 XX XX (SCHD) SCHERING AG.
 XX PI Blume F, Dinkelborg L, Hilger C, Speck U;
 XX DR WPI; 1998-363559/32.
 XX PT Therapeutic use, e.g. in treatment of atherosclerosis, of endothelin
 XX PT conjugates - which comprise residue which can bind endothelin
 XX PT receptor, conjugated to groups such as radionuclides or protein
 XX PT tyrosine kinase blockers
 XX PS Claim 3; Page 15; 21pp; German.
 XX CC The invention relates to (A) the use of conjugates of the following
 XX CC formula as therapeutic agents: E-Wn; where E = a residue which can bind
 XX CC an endothelin receptor, and is derived from an endothelin, an endothelin
 XX CC analogue, an endothelin derivative, an endothelin partial sequence or an
 XX CC endothelin antagonist; W = an active group which: (i) is a radionuclide
 XX CC or (ii) is derived from a chemotherapeutic agent, a complex with a peptide,
 XX CC radioactive metal isotope, an antibody, an antibody fragment, a peptide,
 XX CC a carbohydrate, an oligonucleotide, a protein tyrosine kinase blocker, an
 XX CC anti-thrombotic agent, a coagulation cascade inhibitor, a hormone, growth
 XX CC factor inhibitor, a medicament, a thrombocyte aggregation inhibitor, an
 XX CC anti-inflamatory, a calcium antagonist, a lipid lowering agent or an
 XX CC anti-proliferative agent; n = 1-100, especially 1-10, and (B) conjugates
 XX CC of the above formula in which W is an active group which: (i) is a
 XX CC radionuclide of the elements At, Ba, Br, C, F, N, O or P or (ii) is
 XX CC derived from a chemotherapeutic agent, an oligonucleotide, a protein tyrosine kinase
 XX CC peptide, a carbohydrate, an oligonucleotide, a protein tyrosine kinase
 XX CC blocker, an anti-thrombotic agent, a growth factor inhibitor, a
 XX CC inflammatory, a calcium antagonist, a lipid lowering agent or an anti-
 XX CC proliferative agent. The conjugates may be used as therapeutic agents,
 XX CC especially for treatment of cardiovascular disorders such as
 XX CC atherosclerosis. They may be used in treatment of asthma, cerebral
 XX CC infarction, subarachnoid haemorrhage, preclampsia, renal disorders, etc.
 XX CC The conjugates become enriched in cells in which endothelin receptors
 XX CC are expressed. Even at low doses a therapeutically effective enrichment
 XX CC of the active agent at desired sites can be achieved. Unbound conjugate
 XX CC is rapidly eliminated from the body, reducing side effects. The present
 XX CC sequence represents a specifically claimed endothelin receptor binding
 XX CC peptide which forms part of the conjugate.
 XX SQ Sequence 5 AA;
 XX Query Match 65.2%; Score 15; DB 19; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 4 LW 5
 DB 4 LW 5
 RESULT 69
 ID AAW50857
 AC AAW50857;
 XX 31-JUL-1998 (first entry)
 DE Cyclic peptide which mimics surface feature of endothelin.
 KW Endothelin; endothelina; endothelinb; Eta; ETb; receptor;
 XX Endothelin-1; cyclic.
 XX Synthetic.

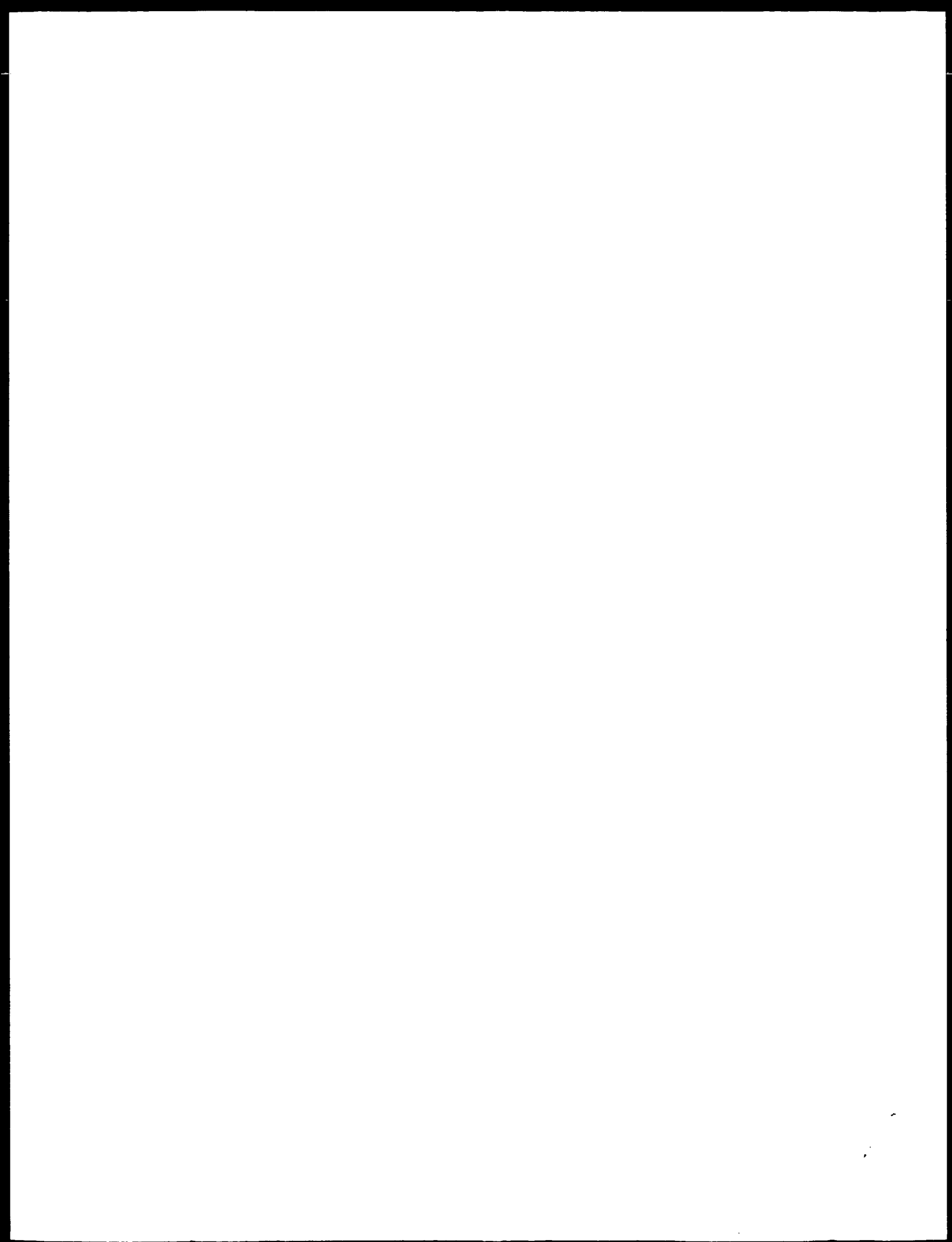

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XX PR 14-MAR-1994; 94US-0212546.
XX PR 15-JAN-1991; 91US-0641720.
XX PR 13-OCT-1992; 92US-0959560.
XX PR 01-JUN-1993; 93US-0069831.
XX PR 12-NOV-1996; 96US-0747137.
XX PA (HEMO-) HEMOSPHERE INC.
XX PI Yen RCK;
XX DR WPI; 1999-508153/42.
XX PT Non-crosslinked protein particles for therapeutic and diagnostic use
XX PS Example 22; Column 65-66; 65pp; English.
XX CC This invention describes a novel aqueous suspension of monodisperse
XX CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
XX CC is stable against dissolving upon dilution with an alcohol-free aqueous
XX CC medium. The method involves (a) forming an aqueous solution containing
XX CC albumin and hemoglobin and (b) treating the aqueous solution with an
XX CC alcohol to cause the solution to become turbid. The particles are useful
XX CC as agents for in vivo administration, either of their own administration
XX CC or as a vehicle for other therapeutic or diagnostic agents. The method
XX CC permits the formation of albumin and hemoglobin particles in the
XX CC nanometer and micrometer size range, in a form closer to their natural
XX CC form than the forms of the prior art. The particles therefore constitute
XX CC a more closely controlled agent for in vivo administration, with greater
XX CC ease of clearance from the body after their period of usefulness.
XX CC AAY30952-Y31135 represent peptides used in the method of the invention.
XX SQ Sequence 5 AA;
XX
Query Match 65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
Db 2 LW 3
XX
RESULT 72
AAY31277
ID AAY31277 standard; peptide; 5 AA.
XX AC AAY31277;
XX DT 28-SEP-1999 (first entry)
XX DE Acetyl choline (muscarinic) GPCR consensus peptide motif.
XX KW Gene characterization; recombinase; homology clamp; homology motif tag;
XX KW HMT; genetic manipulation; genetic engineering; gene transcription; GPCR;
XX KW drug target; homologous recombination; target identification; TGF-beta;
XX KW G-protein coupled receptor; transforming growth factor-beta.
XX OS Homo sapiens.
XX PN WO9937755-A2.
XX PD 29-JUL-1999.
XX PF 11-DEC-1998; 98WO-US26498.
XX PR 11-DEC-1997; 97US-0070734.
XX PA (PANG-) PANGENE CORP.
XX PI Bahman CW, Pati S, Zarling D, Zeng H;
XX DR WPI; 1999-458689/38.
XX
New compositions and methods for targeting sequence modifications in
related family genes
Disclosure; Fig 1A; 46pp; English.
The invention provides compositions and methods for the evaluation and
characterisation of individual and sets of genes in disease states. The
composition comprises at least one recombinase and at least two single-
stranded targeting polynucleotides which are substantially complementary
to each other and each having a consensus homology clamp for a gene
family i.e. a homology motif tag (HMT). The composition is useful in kit
form which include the composition as libraries or pools of degenerate
cSSDNA probes along with other reagents such as recombinase etc. The
methods and compositions are used for inactivation of a gene family gene
i.e. exogenous targeting polynucleotides can be used to inactivate,
decrease or alter the biological activity of one or more genes in a cell
(or transgenic nonhuman animal or plant). This is useful for generating
animal models of disease, or in the elucidation of gene function and
activity. Alternatively, the biological activity of the wild-type gene
may be either decreased or the wild-type activity altered to mimic
disease states. This includes genetic manipulation of non-coding gene
sequences that affect the transcription of genes, including promoter,
repressors, enhancers and transcriptional activating sequences. The
compositions are useful in identifying new members of gene families
which may be useful in functional genomic studies as well as in
identification of new drug targets. HMTs used in homologous recombination
methods can generate animals that have a wide variety of mutations in a
wide variety of related genes, potentially resulting in a wide variety of
phenotypes including those related to disease states. This may also be
done on a cellular level to identify genes involved in cellular
phenotypes i.e. target identification. Sequences AAY31248-308 represent
consensus peptide motifs of the G-protein coupled receptor (GPCR) gene
family and transforming growth factor-beta (TGF-beta) gene family.
XX SQ Sequence 5 AA;
XX
Query Match 65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
Db 3 LW 4
XX
RESULT 73
AAY01560
ID AAY01560 standard; peptide; 5 AA.
XX AC AAY01560;
XX DT 18-JUN-1999 (first entry)
XX DE Antigenic peptide of streptokinase.
XX KW Antigenic peptide; streptokinase; streptokinase-specific antibody;
XX KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
XX KW rheumatic fever.
XX OS Streptococcus equisimilis.
XX PN WO9908698-A1.
XX PD 25-FEB-1999.
XX PF 18-AUG-1998; 98WO-US17114.
XX PR 18-AUG-1997; 97US-0055911.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (HARD ) HARVARD COLLEGE.
XX

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PI Parhami-Seren B, Reed GL;
 XX WPI; 1999-190113/16.
 XX New polypeptides which bind streptokinase-specific antibodies -
 PT useful in thrombolytic therapy
 XX Example 1; Page 24; 44pp; English.
 XX The present sequence represents an antigenic peptide of streptokinase.
 CC The specification describes a polypeptide which binds to a
 CC streptokinase-specific antibody and prevents the antibody binding to
 CC native streptokinase. The specification also describes a synthetic
 CC polypeptide (PI) comprising an epitope which binds to an
 CC streptokinase-specific antibody and reduces thrombolytic activity
 CC of streptokinase. PI is used in thrombolytic therapy, and to
 CC prevent or treat glomerulonephritis and rheumatic fever.
 XX Sequence 5 AA;
 SQ
 Query Match 65.2%; Score 15; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 3 LW 4
 RESULT 74
 AAW99381
 ID AAW99381 standard; peptide; 5 AA.
 AC AAW99381;
 XX 21-MAY-1999 (first entry)
 DT Fibrinogen peptide B(beta)123-127.
 XX Antibody; epitope; trypsin; human; fibrinogen; detection; enzyme;
 KW cleavage; thrombosis; thrombus; thrombolysis.
 XX Homo sapiens.
 OS
 XX WO9905261-A1.
 PN 04-FEB-1999.
 PD 22-JUL-1998; 98WO-US15227.
 PF 25-JUL-1997; 97US-0900895.
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 PA Bini A, Kudryk B;
 PI WPI; 1999-142920/12.
 XX New monospecific antibody to fibrin(ogen) - which can selectively
 PT bind matrix metalloproteinase-mediated cleavage fragments of fibrin
 PT or fibrinogen
 PS Claim 1; Page 34; 75pp; English.
 XX The invention relates to a monospecific antibody that binds specifically
 CC with an epitope defined by the amino acid sequence shown here. The
 CC peptide corresponds to a fragment of a trypsin-digested human fibrinogen
 CC and is designated fragment B(beta)123-127. The antibody can be used for
 CC detecting and measuring enzyme-mediated breakdown of fibrinogen and
 CC fibrin. The specific detection of cleavage products of fibrin and
 CC fibrinogen permits the accurate and precise determination of thrombotic
 CC activity in individuals. The products can be used to study thrombus
 CC development and thrombolysis.

XX
 SQ Sequence 5 AA;
 Query Match 65.2%; Score 15; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 2 LW 3
 RESULT 75
 AAB52657
 ID AAB52657 standard; Peptide; 5 AA.
 AC AAB52657;
 XX 23-FEB-2001 (first entry)
 DT T20/DP178 peptide fragment #35.
 DE Antiinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;
 KW chemoattractant.
 XX Human immunodeficiency virus type 1.
 OS
 XX WO200066622-A1.
 PN 09-NOV-2000.
 PD 05-MAY-2000; 2000WO-US12371.
 PF 05-MAY-1999; 99US-0132686.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
 PI WPI; 2000-656493/63.
 XX Administration of peptide agents with a sequence corresponding to a
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor
 PT antagonist is used to modulate inflammation -
 XX Claim 12; Page 24; 148pp; English.
 XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is
 CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178
 CC interacts with members of the formyl peptide receptor (FPR) family and
 CC thereby up-regulates an inflammatory response, and acts as a potent
 CC chemoattractant and activator of human peripheral blood phagocytes
 CC (but not T cells). The present peptide can be used to modulate an
 CC inflammatory response in a subject.
 XX Sequence 5 AA;
 SQ
 Query Match 65.2%; Score 15; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LW 5
 DB 1 LW 2
 Search completed: February 12, 2003, 10:51:37
 Job time : 82 secs



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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:52:34 ; Search time 29 Seconds
(without alignments)
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Title: US-09-403-440A-1

Perfect score: 23

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 2165

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pap:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pap:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	82.6	5	10	US-09-214-371-2
2	19	82.6	5	10	US-09-281-717-3
3	15	65.2	5	8	US-08-424-550B-228
4	15	65.2	5	10	US-09-841-132-9
5	13	56.5	5	9	US-09-968-561A-211
6	13	56.5	5	9	US-09-968-561A-217
7	13	56.5	5	9	US-09-201-396-7
8	13	56.5	5	9	US-10-105-930-70
9	13	56.5	5	9	US-09-903-412-51
10	13	56.5	5	10	US-09-096-749A-51
11	13	56.5	5	10	US-09-192-854-120
12	13	56.5	5	10	US-09-924-703-9
13	12	52.2	5	8	US-08-239-765B-4
14	12	52.2	5	10	US-09-096-749A-94
15	12	52.2	5	10	US-09-866-135-1
16	11	47.8	5	8	US-08-484-409-35
17	11	47.8	5	8	US-08-424-550B-469
18	11	47.8	5	9	US-09-995-749A-14
19	11	47.8	5	9	US-09-764-884-2

93 11 47.8 5 9 US-09-903-412-69 Sequence 69, Appl
94 11 47.8 5 9 US-09-903-412-74 Sequence 74, Appl
95 11 47.8 5 9 US-09-903-412-76 Sequence 76, Appl
96 11 47.8 5 9 US-09-903-412-78 Sequence 78, Appl
97 11 47.8 5 9 US-09-903-412-80 Sequence 80, Appl
98 11 47.8 5 9 US-09-903-412-82 Sequence 82, Appl
99 11 47.8 5 9 US-09-903-412-84 Sequence 84, Appl
100 11 47.8 5 9 US-09-903-412-86 Sequence 86, Appl

ALIGNMENTS

RESULT 1

US-09-214-371-2
; Sequence 2, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickaley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Where Xaa may be any amino acid
US-09-214-371-2

Query Match 82.6%; Score 19; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | | | |
Db 1 FXXLW 5

RESULT 2

US-09-281-717-3
; Sequence 3, Application US/09281717
; Patent No. US20020061539A1
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)-(3)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

Query Match 82.6%; Score 19; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | | | |
Db 1 FXXLW 5

RESULT 3

US-08-424-550B-228
; Sequence 228, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 4

US-09-841-132-9
; Sequence 9, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841.132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-9

Query Match 65.2%; Score 15; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 5

US-09-968-561A-211
; Sequence 211, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968.561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-211

Query Match 56.5%; Score 13; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 4 MW 5

RESULT 6

US-09-968-561A-217
; Sequence 217, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968.561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-217

Query Match 56.5%; Score 13; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 4 MW 5

RESULT 7

US-09-201-396-7
; Sequence 7, Application US/09201396A
; Publication No. US20030009022A1
; GENERAL INFORMATION:
; APPLICANT: Klein, Christine A.
; APPLICANT: Murphy, Andrew J.
; APPLICANT: Paul, Jeremy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING RECEPTOR
; TITLE OF INVENTION: EFFECTORS
; FILE REFERENCE: CPI-012CP9
; CURRENT APPLICATION NUMBER: US/09/201.396A
; CURRENT FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: 08/582,333
; EARLIER FILING DATE: 1996-01-17
; EARLIER APPLICATION NUMBER: 08/322,137
; EARLIER FILING DATE: 1994-10-13
; EARLIER APPLICATION NUMBER: 08/309,313
; EARLIER FILING DATE: 1994-09-20
; EARLIER APPLICATION NUMBER: 08/190,328
; EARLIER FILING DATE: 1994-01-31
; EARLIER APPLICATION NUMBER: 08/041,431
; EARLIER FILING DATE: 1993-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-201-396-7

Query Match 56.5%; Score 13; DB 9; Length 5;

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Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   :|
Db 2 MW 3

RESULT 8
US-10-105-930-70
; Sequence 70, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-70

Query Match 56.5%; Score 13; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   :|
Db 3 MW 4

RESULT 9
US-09-903-412-51
; Sequence 51, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence of the BC loop of clone pLB24.2.
US-09-903-412-51

Query Match 56.5%; Score 13; DB 9; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   :|
Db 2 MW 3

RESULT 10
US-09-096-749A-51
; Sequence 51, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-09-096-749A-51

Query Match 56.5%; Score 13; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   :|
Db 2 MW 3

RESULT 11
US-09-192-854-120
; Sequence 120, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-192-854-120

Query Match 56.5%; Score 13; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 4 MW 5

RESULT 12

US-09-924-703-9
; Sequence 9, Application US/09924703
; Patent No. US20020137898A1
; GENERAL INFORMATION:
; APPLICANT: TRINCHIERI, GIORGIO
; APPLICANT: PERUSSIA, BICE
; APPLICANT: CLARK, STEVEN C.
; APPLICANT: WONG, GORDON G.
; APPLICANT: HEWICK, RODNEY
; APPLICANT: KOBAYASHI, MICHIO
; TITLE OF INVENTION: ANTIBODIES TO NATURAL KILLER STIMULATORY FACTOR
; FILE REFERENCE: 01142.0142.0100
; CURRENT APPLICATION NUMBER: US/09/924,703
; CURRENT FILING DATE: 2001-08-09
; PRIOR FILING DATE: 09/325,958
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/858,000
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 08/403,013
; PRIOR FILING DATE: 1995-03-13
; PRIOR APPLICATION NUMBER: 07/584,941
; PRIOR FILING DATE: 1990-09-18
; PRIOR APPLICATION NUMBER: 07/307,817
; PRIOR FILING DATE: 1989-02-07
; PRIOR APPLICATION NUMBER: 07/269,945
; PRIOR FILING DATE: 1988-11-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-924-703-9

Query Match 56.5%; Score 13; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 1 IW 2

RESULT 13

US-08-239-765B-4
; Sequence 4, Application US/08239765B
; Patent No. US2002026650A1
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington

; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,765B
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,237
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BT92-01Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-239-765B-4

Query Match 52.2%; Score 12; DB 8; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 2 VW 3

RESULT 14

US-09-096-749A-94
; Sequence 94, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061

```

; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 5 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
;   ORIGINAL SOURCE:
;     US-09-096-749A-94
;
; Query Match          52.2%; Score 12; DB 10; Length 5;
; Best Local Similarity 50.0%; Pred. No. 1.2e+05;
; Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy      4 LW 5
       1
Db      2 VW 3
       1
;
; RESULT 15
; US-09-866-135-1
; Sequence 1, Application US/09866135
; Patent No. US20020051443A1
; GENERAL INFORMATION:
;   APPLICANT: PTITSYN, Leonid R
;   APPLICANT: ALTMAN, Irina B
;   APPLICANT: SMIRNOV, Sergey V
;   APPLICANT: ROSTOVA, Yulia G
;   APPLICANT: YAMPOLSKAYA, Tatyana A
;   APPLICANT: LEONOVA, Tatyana V
;   APPLICANT: GUSVATINER, Mikhail M
;   TITLE OF INVENTION: NEW MUTANT-ACETYLGLUTAMATE SYNTHASE AND METHOD FOR L-ARGININE PRO
;   FILE REFERENCE: 209873US0
;   CURRENT APPLICATION NUMBER: US/09/866,135
;   CURRENT FILING DATE: 2001-06-22
;   PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2000116481
;   PRIOR FILING DATE: 2000-06-28
;   PRIOR APPLICATION NUMBER: RUSSIAN FEDERATION 2001112869
;   PRIOR FILING DATE: 2001-05-15
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 1
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
;
; US-09-866-135-1
;
; Query Match          52.2%; Score 12; DB 10; Length 5;
; Best Local Similarity 50.0%; Pred. No. 1.2e+05;
; Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
Qy      4 LW 5
       1
Db      2 VW 3
       1
;
; RESULT 16
; US-08-484-409-35
; Sequence 35, Application US/08484409
; Patent No. US20020076412A1
; GENERAL INFORMATION:
;   APPLICANT: Steinman, Lawrence
;   APPLICANT: Zamvil, Scott
;   TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SEED and BERRY LLP
;     STREET: 6300 Columbia Center, 701 Fifth Avenue

```

```

; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/484,409
;     FILING DATE: 07-JUN-1995
;     CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Maki, David J.
;     REGISTRATION NUMBER: 31,392
;     REFERENCE/DOCKET NUMBER: 690068,409C1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (206) 622-4900
;     TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 5 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     US-08-484-409-35
;
; Query Match          47.8%; Score 11; DB 8; Length 5;
; Best Local Similarity 100.0%; Pred. No. 1.2e+05;
; Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy      5 W 5
       1
Db      2 W 2
       1
;
; RESULT 17
; US-08-424-550B-469
; Sequence 469, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
;   APPLICANT: JOHN N. SIMONS
;   APPLICANT: TAMI J. PILOT-MATIAS
;   APPLICANT: GEORGE J. DAWSON
;   APPLICANT: GEORGE G. SCHLAUDER
;   APPLICANT: SURESH M. DESAI
;   APPLICANT: THOMAS P. LEARY
;   APPLICANT: ANTHONY SCOTT MUERHOFF
;   APPLICANT: JAMES C. ERKER
;   APPLICANT: SHERI L. BULJK
;   APPLICANT: ISA K. MUSHAWAR
;   TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
;   TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
;   NUMBER OF SEQUENCES: 716
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
;     STREET: 100 ABBOTT PARK ROAD
;     CITY: ABBOTT PARK
;     STATE: IL
;     COUNTRY: USA
;     ZIP: 60064-3500
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/424,550B
;     FILING DATE:
;     CLASSIFICATION: 435435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: POREBSKI, PRISCILLA E.

```

; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 469:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-469

Query Match 47.8%; Score 11; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 5 W 5

RESULT 18

US-09-995-749A-14
; Sequence 14, Application US/09995749A
; Patent No. US20020155568A1
; GENERAL INFORMATION:
; APPLICANT: VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
; APPLICANT: DIJKHUIZEN, LUBBERT
; APPLICANT: RAHOUI, HAKIM
; APPLICANT: LEER, ROBERT-JAN
; TITLE OF INVENTION: NOVEL GLUCOSYLTRANSFERASES
; FILE REFERENCE: B043388-CIP
; CURRENT APPLICATION NUMBER: US/09/995,749A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 09/604,957
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: EPO 00201871.1
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Neisseria polysaccharea
US-09-995-749A-14

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 2 W 2

RESULT 19

US-09-764-884-2
; Sequence 2, Application US/09764884
; Patent No. US20020161208A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT203
; CURRENT APPLICATION NUMBER: US/09/764,884
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-884-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 W 1

RESULT 20

US-09-895-593-15
; Sequence 15, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz
; APPLICANT: Levin, Steven D.
; APPLICANT: Farr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Type I
; OTHER INFORMATION: cytokine receptor conserved motif
; NAME/KEY: UNSURE
; LOCATION: (3)
; OTHER INFORMATION: "Xaa" can be any naturally occurring amino acid
US-09-895-593-15

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 W 1

RESULT 21

US-09-895-593-16
; Sequence 16, Application US/09895593
; Patent No. US20020160949A1
; GENERAL INFORMATION:
; APPLICANT: Pandey, Akhilesh
; APPLICANT: Ozaki, Katsutoshi
; APPLICANT: Baumann, Heinz
; APPLICANT: Levin, Steven D.
; APPLICANT: Farr, Andrew G.
; APPLICANT: Ziegler, Steven F.
; APPLICANT: Leonard, Warren J.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Thymic Stromal Lymphopoietin Receptor Molecules and
; TITLE OF INVENTION: Uses Thereof
US-09-895-593-16

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; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
; OTHER INFORMATION: replacing type I cytokine receptor conserved motif
; OTHER INFORMATION: in murine TSLPR polypeptide
US-09-895-593-16

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 22
US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIAKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-62

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      3 W 3

RESULT 23
US-09-764-857-2
; Sequence 2, Application US/09764857
; Patent No. US20020164685A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ11
; CURRENT APPLICATION NUMBER: US/09/764,857
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 13

; FILE REFERENCE: 00-514-E
; CURRENT APPLICATION NUMBER: US/09/895,593
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/215,658
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-857-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 24
US-09-860-670-2
; Sequence 2, Application US/09860670
; Patent No. US20020165137A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA127P1
; CURRENT APPLICATION NUMBER: US/09/860,670
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-860-670-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 25
US-09-981-876-2
; Sequence 2, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
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PRIOR FILING DATE:	1997-03-07
PRIOR APPLICATION NUMBER:	60/040,334
PRIOR FILING DATE:	1997-03-07
PRIOR APPLICATION NUMBER:	60/040,336
PRIOR FILING DATE:	1997-03-07
PRIOR APPLICATION NUMBER:	60/040,163
PRIOR FILING DATE:	1997-03-07
PRIOR APPLICATION NUMBER:	60/047,615
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,600
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,597
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,502
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,633
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,583
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,617
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,618
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,503
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,592
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,581
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,584
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,500
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,587
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,492
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,598
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,613
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,582
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,596
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,612
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,632
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/047,601
PRIOR FILING DATE:	1997-05-23
PRIOR APPLICATION NUMBER:	60/043,580
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,568
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,314
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,569
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,311
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,671
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,674
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,669
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,312
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,313
PRIOR FILING DATE:	1997-04-11
PRIOR APPLICATION NUMBER:	60/043,672
PRIOR FILING DATE:	1997-04-11

6	PRIOR APPLICATION NUMBER: 60/043,313
7	PRIOR FILING DATE: 1997-04-11
8	PRIOR APPLICATION NUMBER: 60/048,974
9	PRIOR FILING DATE: 1997-06-06
10	PRIOR APPLICATION NUMBER: 60/056,886
11	PRIOR FILING DATE: 1997-08-22
12	PRIOR APPLICATION NUMBER: 60/056,877
13	PRIOR FILING DATE: 1997-08-22
14	PRIOR APPLICATION NUMBER: 60/056,889
15	PRIOR FILING DATE: 1997-08-22
16	PRIOR APPLICATION NUMBER: 60/056,893
17	PRIOR FILING DATE: 1997-08-22
18	PRIOR APPLICATION NUMBER: 60/056,630
19	PRIOR FILING DATE: 1997-08-22
20	PRIOR APPLICATION NUMBER: 60/056,878
21	PRIOR FILING DATE: 1997-08-22
22	PRIOR APPLICATION NUMBER: 60/056,882
23	PRIOR FILING DATE: 1997-08-22
24	PRIOR APPLICATION NUMBER: 60/056,662
25	PRIOR FILING DATE: 1997-08-22
26	PRIOR APPLICATION NUMBER: 60/056,872
27	PRIOR FILING DATE: 1997-08-22
28	PRIOR APPLICATION NUMBER: 60/056,882
29	PRIOR FILING DATE: 1997-08-22
30	PRIOR APPLICATION NUMBER: 60/056,637
31	PRIOR FILING DATE: 1997-08-22
32	PRIOR APPLICATION NUMBER: 60/056,903
33	PRIOR FILING DATE: 1997-08-22
34	PRIOR APPLICATION NUMBER: 60/056,888
35	PRIOR FILING DATE: 1997-08-22
36	PRIOR APPLICATION NUMBER: 60/056,879
37	PRIOR FILING DATE: 1997-08-22
38	PRIOR APPLICATION NUMBER: 60/056,880
39	PRIOR FILING DATE: 1997-08-22
40	PRIOR APPLICATION NUMBER: 60/056,894
41	PRIOR FILING DATE: 1997-08-22
42	PRIOR APPLICATION NUMBER: 60/056,911
43	PRIOR FILING DATE: 1997-08-22
44	PRIOR APPLICATION NUMBER: 60/056,636
45	PRIOR FILING DATE: 1997-08-22
46	PRIOR APPLICATION NUMBER: 60/056,874
47	PRIOR FILING DATE: 1997-08-22
48	PRIOR APPLICATION NUMBER: 60/056,910
49	PRIOR FILING DATE: 1997-08-22
50	PRIOR APPLICATION NUMBER: 60/056,864
51	PRIOR FILING DATE: 1997-08-22
52	PRIOR APPLICATION NUMBER: 60/056,631
53	PRIOR FILING DATE: 1997-08-22
54	PRIOR APPLICATION NUMBER: 60/056,845
55	PRIOR FILING DATE: 1997-08-22
56	PRIOR APPLICATION NUMBER: 60/056,892
57	PRIOR FILING DATE: 1997-08-22
58	PRIOR APPLICATION NUMBER: 60/047,595
59	PRIOR FILING DATE: 1997-05-23
60	PRIOR APPLICATION NUMBER: 60/057,761
61	PRIOR FILING DATE: 03-Sep-1997
62	PRIOR APPLICATION NUMBER: 60/047,599
63	PRIOR FILING DATE: 1997-05-23
64	PRIOR APPLICATION NUMBER: 60/047,588
65	PRIOR FILING DATE: 1997-05-23
66	PRIOR APPLICATION NUMBER: 60/047,585
67	PRIOR FILING DATE: 1997-05-23
68	PRIOR APPLICATION NUMBER: 60/047,586
69	PRIOR FILING DATE: 1997-05-23
70	PRIOR APPLICATION NUMBER: 60/047,590
71	PRIOR FILING DATE: 1997-05-23
72	PRIOR APPLICATION NUMBER: 60/047,594
73	PRIOR FILING DATE: 1997-05-23
74	PRIOR APPLICATION NUMBER: 60/047,589
75	PRIOR FILING DATE: 1997-05-23
76	PRIOR APPLICATION NUMBER: 60/047,593
77	PRIOR FILING DATE: 1997-05-23
78	PRIOR APPLICATION NUMBER: 60/047,614
79	PRIOR FILING DATE: 1997-05-23
80	PRIOR APPLICATION NUMBER: 60/043,578

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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5

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Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5 W 5
        |
Db      1 W 1

```

```

RESULT 26
US-09-984-245-2
; Sequence 2, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30

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; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the L-amino acids commonly found in naturally o
; OTHER INFORMATION: proteins
US-09-984-245-2

```

```

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      5 W 5
        |
Db      1 W 1

```

```

RESULT 27
US-09-764-868-2
; Sequence 2, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PYZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

```

; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-868-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 28

US-10-014-485A-79
; Sequence 79, Application US/10014485A
; Patent No. US20020168684A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: COMB, Michael J.
; APPLICANT: ZHANG, Hui
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U
; FILE OF INVENTION: PEPTIDE LIBRARIES AS ANTIGENS
; FILE REFERENCE: CST-138 CIP2
; CURRENT APPLICATION NUMBER: US/10/014,485A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 3 is phosphorylated
US-10-014-485A-79

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 2 W 2

RESULT 29

US-10-104-019-42
; Sequence 42, Application US/10104019
; Patent No. US20020168379A1
; GENERAL INFORMATION:
; APPLICANT: PAUL, Prem
; APPLICANT: MENG, Xiang-Jin
; APPLICANT: MOROZOV, Igor
; APPLICANT: HALBUR, Patrick
; TITLE OF INVENTION: PROTEINS ENCODED BY POLYNUCLEIC ACIDS OF PORCINE
; FILE REFERENCE: 4625-0039-55X CIP
; CURRENT APPLICATION NUMBER: US/10/104,019
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/019,793
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 08/301,435
; PRIOR FILING DATE: 1994-09-01
; PRIOR APPLICATION NUMBER: 08/131,625

; PRIOR FILING DATE: 1993-10-05
; PRIOR APPLICATION NUMBER: 07/969,071
; PRIOR FILING DATE: 1992-10-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide
US-10-104-019-42

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 30

US-09-764-904-2
; Sequence 2, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI22
; CURRENT APPLICATION NUMBER: US/09/764,904
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-764-904-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 31

US-09-852-797-2
; Sequence 2, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-852-797-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 32
US-09-964-992A-11
; Sequence 11, Application US/09964992A
; Patent No. US20020173633A1
; GENERAL INFORMATION:
; APPLICANT: Campos, Mikal E.
; APPLICANT: No. US20020173633A1ogaki, Hiroyuki
; APPLICANT: Suslow, Trevor
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Characterization of Phenylalanine Ammonia-Lyase (PAL)
; FILE REFERENCE: 023070-124500US
; CURRENT APPLICATION NUMBER: US/09/964,992A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/235,956
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PAL conserved
; OTHER INFORMATION: peptide fragment
US-09-964-992A-11

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 33
US-10-035-349-2
; Sequence 2, Application US/10035349
; Patent No. US20020172961A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Luke V.
; APPLICANT: Hall, Michael P.
; APPLICANT: Petesch, Robert
; APPLICANT: Target Discovery, Inc.
; TITLE OF INVENTION: Mass Defect Labeling for the Determination of Oligomer
; FILE REFERENCE: 020444-000710US
; CURRENT APPLICATION NUMBER: US/10/035,349
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/242,165
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/242,398
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: competing 5
; OTHER INFORMATION: residue false sequence, top ranked sequence at
; OTHER INFORMATION: five residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = Gly labeled with 5-bromo-3-pyridylacetic
; OTHER INFORMATION: acid (5-Br-3-PAA)
US-10-035-349-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 34
US-10-035-349-8
; Sequence 8, Application US/10035349
; Patent No. US20020172961A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Luke V.
; APPLICANT: Hall, Michael P.
; APPLICANT: Petesch, Robert
; APPLICANT: Target Discovery, Inc.
; TITLE OF INVENTION: Mass Defect Labeling for the Determination of Oligomer
; FILE REFERENCE: 020444-000710US
; CURRENT APPLICATION NUMBER: US/10/035,349
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/242,165
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/242,398
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: competing 5
; OTHER INFORMATION: residue false sequence, top ranked sequence at
; OTHER INFORMATION: five residues
US-10-035-349-8

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 35
US-09-828-272A-6
; Sequence 6, Application US/09828272A
; Publication No. US20020183255A1
; GENERAL INFORMATION:
; APPLICANT: LIPTON, James M
; APPLICANT: CATANIA, Anna P
; TITLE OF INVENTION: USE OF KP V TRIPEPTIDE FOR DERMATOLOGICAL DISORDERS
; FILE REFERENCE: 259/058
; CURRENT APPLICATION NUMBER: US/09/828,272A
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed polypeptide with anti-inflammatory, anti-bacterial, anti
; OTHER INFORMATION: -fungal and antipyretic properties.

US-09-828-272A-6

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 36
US-10-042-141-2
; Sequence 2, Application US/10042141
; Publication No. US20020183503A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 26 Human secreted proteins
; FILE REFERENCE: P2040P1
; CURRENT APPLICATION NUMBER: US/10/042,141
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/726,643
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/15187
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,725
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-042-141-2

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 1 W 1

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 1 W 1

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 1 W 1

Qy 5 W 5
|
Db 1 W 1

RESULT 37
US-10-059-749-57
; Sequence 57, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-059-749-57

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; Indels 0; Gaps 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 38
US-10-059-749-63
; Sequence 63, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP

```

; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 63:
;
; US-10-059-749-63

```

```

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 W 5
   |
Db 1 W 1

```

```

RESULT 39
US-10-059-749-69
; Sequence 69, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; FERNANDES-ALNEMRI, TERESA
; Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
;
; US-10-059-749-69

```

```

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 5 W 5
   |
Db 1 W 1

```

```

RESULT 40
US-10-079-625-6
; Sequence 6, Application US/10079625
; Publication No. US20020182676A1
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,625
; FILING DATE: 2002-FEB-19
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.

```

; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-079-625-6

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 41

US-10-029-301-4
; Sequence 4, Application US/10029301
; Publication No. US20020188107A1
; GENERAL INFORMATION:
; APPLICANT: Mmott, Tracy Lehanne
; APPLICANT: Engwerda, Christian
; APPLICANT: Peek, Keith
; TITLE OF INVENTION: Component of Stem Bromelain (as amended)
; FILE REFERENCE: 0623.0760002
; CURRENT APPLICATION NUMBER: US/10/029,301
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/382,689
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/GB98/00592
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: GB 9704252.7
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: GB 9703850.9
; PRIOR FILING DATE: 1997-02-25
; PRIOR APPLICATION NUMBER: GB 9703827.7
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Ananas comosus
US-10-029-301-4

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 2 W 2

RESULT 42

US-10-074-956-6
; Sequence 6, Application US/10074956
; Publication No. US2002019332A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/10/074,956
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/268,175

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-956-6

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 5 W 5

RESULT 43

US-10-078-059-5
; Sequence 5, Application US/10078059
; Publication No. US20020193305A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
; FILE REFERENCE: PF466P2
; CURRENT APPLICATION NUMBER: US/10/078,059
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/269,876
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/22493
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 09/376,430
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 09/263,626
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US99/05068
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 60/086,505
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-078-059-5

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 44

US-10-087-195-3
; Sequence 3, Application US/10087195
; Publication No. US20020193306A1
; GENERAL INFORMATION:
; APPLICANT: Nuttall, Patricia, Anne
; APPLICANT: Faesen, Guido, Christiaan
; TITLE OF INVENTION: Treatment of Allergic Rhinitis
; FILE REFERENCE: 2488-1-004
; CURRENT APPLICATION NUMBER: US/10/087,195

```

; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/GB00/03287
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 9920673.2
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: arthropod
US-10-087-195-3

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      4 W 4

RESULT 45
US-09-320-713-14
; Sequence 14, Application US/09320713
; Publication No. US2003003545A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: x equals any amino acid
US-09-320-713-14

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      1 W 1

RESULT 46
US-09-774-639-2
; Sequence 2, Application US/09774639
; Publication No. US2003003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371

; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/GB00/03287
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 9920673.2
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
US-09-798-889-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      1 W 1

RESULT 47
US-09-798-889-2
; Sequence 2, Application US/09798889
; Publication No. US20030004324A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human secreted proteins
; FILE REFERENCE: P2026P1
; CURRENT APPLICATION NUMBER: US/09/798,889
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,714
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,686
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/077,696
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
US-09-798-889-2

Query Match          47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      1 W 1

RESULT 48
US-10-105-930-21
; Sequence 21, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930

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; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary motif
; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = any amino acid
US-10-105-930-21

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 49
US-10-105-930-57
; Sequence 57, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-57

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 50
US-10-105-930-58
; Sequence 58, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1

; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-58

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 51
US-10-105-930-59
; Sequence 59, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-59

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 52
US-10-105-930-60
; Sequence 60, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-60

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 53
US-10-105-930-61
; Sequence 61, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-61

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 54
US-10-105-930-62
; Sequence 62, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-62

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 55
US-10-105-930-63
; Sequence 63, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-63

Query Match      47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 56
US-10-105-930-64
; Sequence 64, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-64
```

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 57
US-10-105-930-65
; Sequence 65, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-65

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 58
US-10-105-930-66
; Sequence 66, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-66

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 59
US-10-105-930-67
; Sequence 67, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-67

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 60
US-10-105-930-68
; Sequence 68, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1iko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-68

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 61

US-10-105-930-69
 ; Sequence 69, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JP00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 69
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-69

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 62

US-10-105-930-71
 ; Sequence 71, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JP00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 71
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-71

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 63

US-10-105-930-72
 ; Sequence 72, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:

; APPLICANT: Maeda, Masatsugu
 ; APPLICANT: Yaguchi, No. US20030009018A1iko
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JP00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-72

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 64

US-10-105-930-73
 ; Sequence 73, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JP00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 73
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-73

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 65

US-10-105-930-74
 ; Sequence 74, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; APPLICANT: Yaguchi, No. US20030009018A1iko
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105U51
 ; CURRENT APPLICATION NUMBER: US/10/105,930

; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 74
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-74

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 4 W 4

RESULT 66
 US-10-105-930-75
 ; Sequence 75, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105US1
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 75
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-75

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 1 W 1

RESULT 67
 US-10-105-930-76
 ; Sequence 76, Application US/10105930
 ; Publication No. US20030009018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maeda, Masatsugu
 ; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
 ; FILE REFERENCE: 06501-105US1
 ; CURRENT APPLICATION NUMBER: US/10/105,930
 ; CURRENT FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: PCT/JF00/06654
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: JP 2000-240397
 ; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP 11-273358
 ; PRIOR FILING DATE: 1999-09-27
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 76
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-105-930-76

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 1 W 1

RESULT 68
 US-09-262-126C-8
 ; Sequence 8, Application US/09262126C
 ; Publication No. US20030013180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miller, Brian S.
 ; APPLICANT: Shetty, Jayarama K.
 ; TITLE OF INVENTION: Modified Forms of Pullulanase
 ; FILE REFERENCE: GC396-2
 ; CURRENT APPLICATION NUMBER: US/09/262,126C
 ; CURRENT FILING DATE: 1999-03-03
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Unknown
 US-09-262-126C-8

Query Match 47.8%; Score 11; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 3 W 3

RESULT 69
 US-09-989-442-2
 ; Sequence 2, Application US/09989442
 ; Publication No. US20030013649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PJZ08
 ; CURRENT APPLICATION NUMBER: US/09/989,442
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038

; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-09-14
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; PRIOR FILING DATE: 2000-09-08

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;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
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;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065
;; PRIOR FILING DATE: 2000-09-14

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 70
US-10-116-067-3
; Sequence 3, Application US/10116067
; Publication No. US20030012780A1
; GENERAL INFORMATION:
; APPLICANT: LINDBOM, Lennart
; APPLICANT: WERR, Joachim
; TITLE OF INVENTION: Anti-Inflammatory Medicaments
; FILE REFERENCE: 1291-0200P
; CURRENT APPLICATION NUMBER: US/10/116,067
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: SE 9803428-3
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: US 60/103,558
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: PCT/SE99/01801
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: alphabeta1 integrin-binding peptide
US-10-116-067-3

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 5 W 5

RESULT 71
US-09-369-248-5
; Sequence 5, Application US/09369248
; Publication No. US20030022276A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation
; FILE REFERENCE: PF448
; CURRENT APPLICATION NUMBER: US/09/369,248
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/073,962
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/078,572
; EARLIER FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any amino acid
US-09-369-248-5

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 72
US-09-393-696-14
; Sequence 14, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any amino acid
US-09-393-696-14

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 1 w 1

RESULT 73

US-09-747-377-493

Sequence 493, Application US/09747377

Publication No. US20030022255A1

GENERAL INFORMATION:

APPLICANT: Morris David

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

FILE REFERENCE: A-6959/RMS/DCF

CURRENT APPLICATION NUMBER: US/09/747,377

CURRENT FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 493

SOFTWARE: PatentIn version 3.0

SEQ ID NO 493

LENGTH: 5

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Cytokine receptor extracellular motif found in many species.

NAME/KEY: (3)

LOCATION: (3)

OTHER INFORMATION: "Xaa" at position 3 can be any amino acid

US-09-747-377-493

Query Match 47.8%; Score 11; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 w 5

Db 1 w 1

RESULT 74

US-09-983-802-2

Sequence 2, Application US/09983802

Publication No. US20030022185A1

GENERAL INFORMATION:

APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins

FILE REFERENCE: P2010P1

CURRENT APPLICATION NUMBER: US/09/983,802

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684

PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

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PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

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PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661

PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12

NUMBER OF SEQ ID NOS: 672

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 5

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Site

LOCATION: (3)

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

OTHER INFORMATION: acids

US-09-983-802-2

Query Match 47.8%; Score 11; DB 9; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 w 5

Db 1 w 1

RESULT 75

US-10-062-523-5

Sequence 5, Application US/10062523

Publication No. US20030022327A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation

TITLE OF INVENTION: Molecule

FILE REFERENCE: PP448P2

CURRENT APPLICATION NUMBER: US/10/062,523

; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/267,523
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/US00/21130
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/190,062
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/369,248
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: PCT/US99/02415
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/244,110
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/078,572
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/073,962
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-062-523-5

Query Match 47.8%; Score 11; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 W 5
Db 1 W 1

Search completed: February 12, 2003, 10:56:29
Job time : 30 secs

The first of these is the fact that the
 government has been unable to
 maintain a stable currency. This
 has led to a loss of confidence
 in the government and a
 consequent loss of support
 from the people. The second
 is the fact that the government
 has been unable to maintain
 a stable economy. This has
 led to a loss of confidence
 in the government and a
 consequent loss of support
 from the people. The third
 is the fact that the government
 has been unable to maintain
 a stable society. This has
 led to a loss of confidence
 in the government and a
 consequent loss of support
 from the people.

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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:51:44 ; Search time 131 Seconds
(without alignments)
24.608 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 42829

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
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16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
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24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	87.0	5	1	PCT-US99-02405-11
2	20	87.0	5	1	PCT-US99-26277-114
3	20	87.0	5	20	US-09-601-558-11
4	20	87.0	5	22	US-09-831-047B-114
5	20	87.0	5	22	US-09-831-047C-114
6	20	87.0	5	22	US-09-894-594-11

5	1	PCT-US01-20969-3	82.6	19	Sequence 3, Appli
5	16	US-09-214-371-2	82.6	19	Sequence 2, Appli
5	16	US-09-281-717-3	82.6	19	Sequence 3, Appli
5	18	US-09-403-440A-1	82.6	19	Sequence 1, Appli
5	20	US-09-609-361-3	82.6	19	Sequence 3, Appli
5	23	US-09-957-806A-226	82.6	19	Sequence 226, App
5	1	PCT-US01-03988-791	65.2	15	Sequence 791, App
5	1	PCT-US02-22821-139	65.2	15	Sequence 139, App
5	1	PCT-US02-23257-8	65.2	15	Sequence 8, Appli
5	1	PCT-US02-23257-10	65.2	15	Sequence 10, Appli
5	1	PCT-US02-23257-11	65.2	15	Sequence 11, Appli
5	1	PCT-US02-23257-12	65.2	15	Sequence 12, Appli
5	1	PCT-US02-23257-13	65.2	15	Sequence 13, Appli
5	1	PCT-US98-15227-1	65.2	15	Sequence 1, Appli
5	1	PCT-US99-11219-791	65.2	15	Sequence 791, App
5	3	US-07-585-141-11	65.2	15	Sequence 11, Appli
5	3	US-07-608-569-17	65.2	15	Sequence 17, Appli
5	7	US-08-344-185B-100	65.2	15	Sequence 100, App
5	7	US-08-344-185B-454	65.2	15	Sequence 454, App
5	7	US-08-344-185C-100	65.2	15	Sequence 100, App
5	7	US-08-344-185C-454	65.2	15	Sequence 454, App
5	8	US-08-424-550A-228	65.2	15	Sequence 228, App
5	8	US-08-424-550B-228	65.2	15	Sequence 228, App
5	8	US-08-432-147-47	65.2	15	Sequence 47, Appli
5	8	US-08-467-344A-228	65.2	15	Sequence 228, App
5	8	US-08-486-749-228	65.2	15	Sequence 228, App
5	8	US-08-488-445A-228	65.2	15	Sequence 228, App
5	8	US-08-488-446-228	65.2	15	Sequence 228, App
5	9	US-08-530-325-14	65.2	15	Sequence 14, Appli
5	9	US-08-530-327-14	65.2	15	Sequence 14, Appli
5	13	US-08-981-122-15	65.2	15	Sequence 15, Appli
5	13	US-08-981-122-38	65.2	15	Sequence 38, Appli
5	13	US-08-981-122-43	65.2	15	Sequence 43, Appli
5	13	US-08-981-122-51	65.2	15	Sequence 51, Appli
5	16	US-09-209-676-30	65.2	15	Sequence 30, Appli
5	16	US-09-284-327-1	65.2	15	Sequence 1, Appli
5	17	US-09-308-823A-582	65.2	15	Sequence 582, App
5	17	US-09-350-641B-791	65.2	15	Sequence 791, App
5	17	US-09-350-641C-791	65.2	15	Sequence 791, App
5	17	US-09-350-641C-791	65.2	15	Sequence 791, App
5	18	US-09-410-568-9	65.2	15	Sequence 9, Appli
5	18	US-09-426-371-9	65.2	15	Sequence 9, Appli
5	18	US-09-454-684-9	65.2	15	Sequence 9, Appli
5	18	US-09-454-684A-9	65.2	15	Sequence 9, Appli
5	18	US-09-457-198A-25	65.2	15	Sequence 25, Appli
5	19	US-09-515-965-791	65.2	15	Sequence 791, App
5	19	US-09-515-965A-791	65.2	15	Sequence 791, App
5	19	US-09-515-965A-1657	65.2	15	Sequence 1657, Ap
5	19	US-09-536-998-1	65.2	15	Sequence 1, Appli
5	19	US-09-598-419-9	65.2	15	Sequence 9, Appli
5	20	US-09-632-426-30	65.2	15	Sequence 30, Appli
5	20	US-09-632-426-30	65.2	15	Sequence 30, Appli
5	20	US-09-636-243A-75	65.2	15	Sequence 75, Appli
5	20	US-09-642-234-75	65.2	15	Sequence 75, Appli
5	20	US-09-657-276-723	65.2	15	Sequence 723, App
5	20	US-09-657-276-724	65.2	15	Sequence 724, App
5	20	US-09-657-276-734	65.2	15	Sequence 734, App
5	20	US-09-657-276-1560	65.2	15	Sequence 1560, Ap
5	21	US-09-762-270-19	65.2	15	Sequence 19, Appli
5	21	US-09-762-270-20	65.2	15	Sequence 20, Appli
5	21	US-09-762-270-21	65.2	15	Sequence 21, Appli
5	21	US-09-762-270-22	65.2	15	Sequence 22, Appli
5	21	US-09-762-270-23	65.2	15	Sequence 23, Appli
5	22	US-09-834-784-791	65.2	15	Sequence 791, App
5	22	US-09-841-132-9	65.2	15	Sequence 9, Appli
5	23	US-09-920-306-21	65.2	15	Sequence 21, Appli
5	23	US-09-350-369C-513	65.2	15	Sequence 513, App
5	23	US-09-350-369C-1389	65.2	15	Sequence 1389, Ap
5	24	US-10-005-305-36	65.2	15	Sequence 36, Appli
5	24	US-10-005-305-95	65.2	15	Sequence 95, Appli
5	25	US-10-197-954-139	65.2	15	Sequence 139, App
5	26	US-10-200-923-8	65.2	15	Sequence 8, Appli
5	26	US-10-200-923-10	65.2	15	Sequence 10, Appli

Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 65, Appl
Sequence 99, Appl
Sequence 83, Appl
Sequence 169, Appl
Sequence 4, Appl
Sequence 97, Appl
Sequence 75, Appl
Sequence 282, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 47, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 5, Appl
Sequence 47, Appl

ALIGNMENTS

RESULT 1
PCT-US99-02405-11
; Sequence 11, Application PC/TUS9902405
; GENERAL INFORMATION:
; APPLICANT: Trustees of the University of Pennsylvania
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
; FILE REFERENCE: UPN3544
; CURRENT APPLICATION NUMBER: PCT/US99/02405
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 60/073,690
; EARLIER FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US99-02405-11

Query Match 87.0%; Score 20; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| |
Db 1 FSLWL 5

RESULT 2
PCT-US99-26277-114
; Sequence 114, Application PC/TUS9926277
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebler-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93PCT
; CURRENT APPLICATION NUMBER: PCT/US99/26277
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 60/107,478
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen
PCT-US99-26277-114

Query Match 87.0%; Score 20; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| |
Db 1 FSLWL 5

RESULT 3
US-09-601-558-11
; Sequence 11, Application US/09601558
; GENERAL INFORMATION:
; APPLICANT: Kiebler-Emmons, Thomas

; APPLICANT: The Trustees of the University of Pennsylvania
; TITLE OF INVENTION: Peptide Mimotopes Of Carbohydrate Antigens
; FILE REFERENCE: UPN3567
; CURRENT APPLICATION NUMBER: US/09/601,558
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-601-558-11

Query Match 87.0%; Score 20; DB 20; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| |
Db 1 FSLWL 5

RESULT 4
US-09-831-047B-114
; Sequence 114, Application US/09831047B
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebler-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047B
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/107,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen

US-09-831-047B-114

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FSLW 5

RESULT 5

US-09-831-047C-114
; Sequence 114, Application US/09831047C
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kieber-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047C
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/107,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: peptido-mimetic of a Lewis antigen

US-09-831-047C-114

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FSLW 5

RESULT 6

US-09-894-594-11
; Sequence 11, Application US/09894594
; GENERAL INFORMATION:
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatolah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encod
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/601,558
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Novel Sequence

US-09-894-594-11

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FSLW 5

RESULT 7

PCT-US01-20969-3
; Sequence 3, Application PC/TUS0120969
; GENERAL INFORMATION:
; APPLICANT: GUY, RODNEY
; APPLICANT: BAXTER, JOHN
; APPLICANT: DARIMONT, BEATRICE
; APPLICANT: FENG, WEIJUN
; APPLICANT: ROBERT, FLETTERICK
; APPLICANT: PETER, KUSHNER
; APPLICANT: RICHARD, WAGNER
; APPLICANT: BRIAN, WEST
; APPLICANT: YAMAMOTO, KEITH
; APPLICANT: GEISTLINGER, TIMOTHY
; APPLICANT: ARNOLD, JAMES
; APPLICANT: KUNTZ, IRWIN
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; FILE REFERENCE: 9811-016-228
; CURRENT APPLICATION NUMBER: PCT/US01/20969
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/609,361
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/079,965
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US09/281,717
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa is any amino acid

PCT-US01-20969-3

Query Match 82.6%; Score 19; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FXXLW 5

RESULT 8

US-09-214-371-2
; Sequence 2, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picklesley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Scheverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT

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; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: Where Xaa may be any amino acid
US-09-214-371-2

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Query Match      82.6%; Score 19; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FXXLW 5
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Db 1 FXXLW 5

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RESULT 9
US-09-281-717-3
; Sequence 3, Application US/09281717
; GENERAL INFORMATION:
; APPLICANT: Baxter, John D.
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletcher, Robert J.
; APPLICANT: Kushner, Peter J.
; APPLICANT: Wagner, Richard L.
; APPLICANT: West, Brian
; APPLICANT: Yamamoto, Keith R.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: UCAL-253/02US
; CURRENT APPLICATION NUMBER: US/09/281,717
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: US 60/079,956
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-281-717-3

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Query Match      82.6%; Score 19; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FXXLW 5
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Db 1 FXXLW 5

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RESULT 10
US-09-403-440A-1
; Sequence 1, Application US/09403440A
; GENERAL INFORMATION:
; APPLICANT: Lane, David Philip
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO
; TITLE OF INVENTION: INHIBITING THE INTERACTION OF p53 AND MDM2
; FILE REFERENCE: MEWE25.001APC
; CURRENT APPLICATION NUMBER: US/09/403,440A

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; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: PCT/GB98/01144
; PRIOR FILING DATE: 1998-04-20
; PRIOR APPLICATION NUMBER: GB 9708092.3
; PRIOR FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This represents a consensus sequence representing
; OTHER INFORMATION: humans and mice.
; NAME/KEY: UNSURE
; LOCATION: 2, 3
; OTHER INFORMATION: Xaa = any amino acid
US-09-403-440A-1

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```

Query Match      82.6%; Score 19; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 FXXLW 5
   |||||
Db 1 FXXLW 5

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RESULT 11
US-09-609-361-3
; Sequence 3, Application US/09609361
; GENERAL INFORMATION:
; APPLICANT: GUY, RODNEY
; APPLICANT: BAXTER, JOHN
; APPLICANT: DARIMONT, BEATRICE
; APPLICANT: FENG, WEIJUN
; APPLICANT: ROBERT, FLETTERICK
; APPLICANT: PETER, KUSHNER
; APPLICANT: RICHARD, WAGNER
; APPLICANT: BRIAN, WEST
; APPLICANT: YAMAMOTO, KEITH
; APPLICANT: GEISTLINGER, TIMOTHY
; APPLICANT: ARNOLD, JAMES
; APPLICANT: KUNTZ, IRWIN
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR ACTIVITY
; FILE REFERENCE: 9811-016-999
; CURRENT APPLICATION NUMBER: US/09/609,361
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/079,965
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: US 60/113,146
; PRIOR FILING DATE: 1998-12-16
; PRIOR APPLICATION NUMBER: US09/281,717
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa is any amino acid
US-09-609-361-3

```

```

Query Match      82.6%; Score 19; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 FXXLW 5
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Db 1 FXXLW 5

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; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

; FILE OF INVENTION: Compositions

; FILE REFERENCE: 24743-2305

; CURRENT APPLICATION NUMBER: PCT/US02/22821

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 60/306,019

; PRIOR FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/314,123

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 60/363,433

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 139

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo Sapien

; PCT-US02-22821-139

Query Match 65.2%; Score 15; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

Db 2 LW 3

RESULT 15

PCT-US02-23257-8

; Sequence 8, Application PC/TUS0223257

; GENERAL INFORMATION:

; APPLICANT: The Brigham and Women's Hospital, Inc.

; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN

; FILE REFERENCE: 50073/010W02

; CURRENT APPLICATION NUMBER: PCT/US02/23257

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: US 60/307,228

; PRIOR FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

PCT-US02-23257-8

Query Match

65.2%; Score 15; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

Db 4 LW 5

RESULT 16

PCT-US02-23257-10

; Sequence 10, Application PC/TUS0223257

; GENERAL INFORMATION:

; APPLICANT: The Brigham and Women's Hospital, Inc.

; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN

; FILE REFERENCE: 50073/010W02

; CURRENT APPLICATION NUMBER: PCT/US02/23257

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: US 60/307,228

; PRIOR FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

RESULT 12

US-09-957-806A-226

; Sequence 226, Application US/09957806A

; GENERAL INFORMATION:

; APPLICANT: Roggen, Erwin

; APPLICANT: Ernst, Steffen

; APPLICANT: Svendsen, Allan

; APPLICANT: Friis, Esben

; APPLICANT: Osten, Claus

; TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY

; FILE REFERENCE: 10021.204-US

; CURRENT APPLICATION NUMBER: US/09/957,806A

; CURRENT FILING DATE: 2001-09-21

; NUMBER OF SEQ ID NOS: 248

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 226

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Betula

US-09-957-806A-226

Query Match

82.6%; Score 19; DB 23; Length 5;

Best Local Similarity 60.0%; Pred. No. 4.2e+06;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

Db 1 FIKLW 5

RESULT 13

PCT-US01-03988-791

; Sequence 791, Application PC/TUS0103988

; GENERAL INFORMATION:

; APPLICANT: Trimeris, Inc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

; FILE REFERENCE: FUSION-

; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION

; FILE REFERENCE: 7872-073-228

; CURRENT APPLICATION NUMBER: PCT/US01/03988

; CURRENT FILING DATE: 2001-02-07

; PRIOR APPLICATION NUMBER: 09/515,965

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 1589

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 791

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

PCT-US01-03988-791

Query Match

65.2%; Score 15; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.2e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

Db 1 LW 2

RESULT 14

PCT-US02-22821-139

; Sequence 139, Application PC/TUS0222821

; GENERAL INFORMATION:

; APPLICANT: HK Pharmaceuticals, Inc.

; APPLICANT: Koister, Hubert

; APPLICANT: Siddiqi, Suhail

; APPLICANT: Little, Daniel

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-23257-10

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
Db 4 LW 5

RESULT 17
PCT-US02-23257-11
; Sequence 11, Application PC/TUS0223257
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; TITLE OF INVENTION: RECEPTOR LIGANDS
; FILE REFERENCE: 50073/010W02
; CURRENT APPLICATION NUMBER: PCT/US02/23257
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-23257-11

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
Db 4 LW 5

RESULT 18
PCT-US02-23257-12
; Sequence 12, Application PC/TUS0223257
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; TITLE OF INVENTION: RECEPTOR LIGANDS
; FILE REFERENCE: 50073/010W02
; CURRENT APPLICATION NUMBER: PCT/US02/23257
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-23257-12

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
Db 4 LW 5

RESULT 19
PCT-US02-23257-13
; Sequence 13, Application PC/TUS0223257
; GENERAL INFORMATION:
; APPLICANT: The Brigham and Women's Hospital, Inc.
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN
; TITLE OF INVENTION: RECEPTOR LIGANDS
; FILE REFERENCE: 50073/010W02
; CURRENT APPLICATION NUMBER: PCT/US02/23257
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/307,228
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Ile at position 3 is alle
PCT-US02-23257-13

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
Db 4 LW 5

RESULT 20
PCT-US98-15227-1
; Sequence 1, Application PC/TUS9815227
; GENERAL INFORMATION:
; APPLICANT: The New York Blood Center, Inc.
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODY REACTIVE WITH
; TITLE OF INVENTION: MATRIX METALLOPROTEINASE CLEAVAGE PRODUCTS OF FIBRIN(OGEN)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/15227
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/900,895
; FILING DATE: 7/25/97
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 454-16 PCT
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 822-3550
 TELEFAX: (516) 822-3582
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US98-15227-1

Query Match 65.2%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 ||
 DB 2 LW 3

RESULT 21

PCT-US99-11219-791
 ; Sequence 791, Application PC/TUS9911219
 ; GENERAL INFORMATION:
 ; APPLICANT: TRIMERIS, INC.
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
 ; FILE OF INVENTION: PROPERTIES
 ; FILE REFERENCE: 7872-052-228
 ; CURRENT APPLICATION NUMBER: PCT/US99/11219
 ; CURRENT FILING DATE: 1999-05-20
 ; NUMBER OF SEQ ID NOS: 1542
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 791
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 PCT-US99-11219-791

Query Match 65.2%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 ||
 DB 1 LW 2

RESULT 22

US-07-585-141-11
 ; Sequence 11, Application US/07585141
 ; GENERAL INFORMATION:
 ; APPLICANT: Schramm, Wolfgang
 ; APPLICANT: Schramm, Hans J.
 ; TITLE OF INVENTION: Agent For Inhibiting Symmetrical
 ; TITLE OF INVENTION: Proteins, In Particular Enzymes
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/585,141
 ; FILING DATE: 19901009
 ; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/EP90/00219
 ; FILING DATE: 09-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 39 04 040.2
 ; FILING DATE: 10-FEB-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28957
 ; REFERENCE/DOCKET NUMBER: 18644-96040
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: YES
 ; US-07-585-141-11

Query Match 65.2%; Score 15; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 ||
 DB 1 LW 2

RESULT 23

US-07-608-569-17
 ; Sequence 17, Application US/07608569
 ; GENERAL INFORMATION:
 ; APPLICANT: Tainer, John A
 ; APPLICANT: Kuhn, Leslie
 ; APPLICANT: Boissinot, Maurice
 ; APPLICANT: Fisher, Cindy
 ; APPLICANT: Parge, Hans E
 ; APPLICANT: Griffin, John H
 ; APPLICANT: Mullenbach, Guy T
 ; APPLICANT: Hallowell, Robert A
 ; TITLE OF INVENTION: Glycosaminoglycan-Targeted Fusion
 ; TITLE OF INVENTION: Proteins, Their Design, Construction and Compositions
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: The Scripps Research Institute, Office of
 ; ADDRESSEE: Patent Counsel
 ; STREET: 10666 North Torrey Pines Road
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/608,569
 ; FILING DATE: 19901102
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/608539
 ; FILING DATE: 01-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCR0348P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-544-2937
 ; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-07-608-569-17

Query Match 65.2%; Score 15; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 1 LW 2

RESULT 24
 US-08-344-185B-100
 ; Sequence 100, Application US/08344185B
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMONS, JOHN N.
 ; APPLICANT: PILOT-MATIAS, T.J.
 ; APPLICANT: DAWSON, GEORGE J.
 ; APPLICANT: SCHLAUDER, GEORGE G.
 ; APPLICANT: DESAI, SURESH M.
 ; APPLICANT: LEARY, THOMAS P.
 ; APPLICANT: MUEHROFF, ANTHONY T.
 ; APPLICANT: BUIJK, S.L.
 ; APPLICANT: MUSHAWAR, ISA K.
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 539
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/344,185B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOREMSKI, PRISCILLA E.
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 100:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-344-185B-100

Query Match 65.2%; Score 15; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 3 LW 4

RESULT 25

US-08-344-185B-454
 ; Sequence 454, Application US/08344185B
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMONS, JOHN N.
 ; APPLICANT: PILOT-MATIAS, T.J.
 ; APPLICANT: DAWSON, GEORGE J.
 ; APPLICANT: SCHLAUDER, GEORGE G.
 ; APPLICANT: DESAI, SURESH M.
 ; APPLICANT: LEARY, THOMAS P.
 ; APPLICANT: MUEHROFF, ANTHONY T.
 ; APPLICANT: BUIJK, S.L.
 ; APPLICANT: MUSHAWAR, ISA K.
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 539
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/344,185B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOREMSKI, PRISCILLA E.
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 454:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-344-185B-454

Query Match 65.2%; Score 15; DB 7; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 4 LW 5

RESULT 26
 US-08-344-185C-100
 ; Sequence 100, Application US/08344185C
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMONS, JOHN N.
 ; APPLICANT: PILOT-MATIAS, T.J.
 ; APPLICANT: DAWSON, GEORGE J.
 ; APPLICANT: SCHLAUDER, GEORGE G.
 ; APPLICANT: DESAI, SURESH M.
 ; APPLICANT: LEARY, THOMAS P.
 ; APPLICANT: MUEHROFF, ANTHONY T.
 ; APPLICANT: BUIJK, S.L.
 ; APPLICANT: MUSHAWAR, ISA K.
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E
 ; TITLE OF INVENTION: HEPATITIS REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 539
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES
 ; STREET: ONE HUNDRED ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK

; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,185C
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-344-185C-100

Query Match 65.2%; Score 15; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
DB 3 LW 4

RESULT 27
US-08-344-185C-454
; Sequence 454, Application US/08344185C
; GENERAL INFORMATION:
; APPLICANT: SIMONS, JOHN N.
; APPLICANT: PILOT-MATIAS, T.J.
; APPLICANT: DAWSON, GEORGE J.
; APPLICANT: SCHLAUDER, GEORGE G.
; APPLICANT: DESAI, SURESH M.
; APPLICANT: LEARY, THOMAS P.
; APPLICANT: MUEHROFF, ANTHONY T.
; APPLICANT: BUIJK, S.L.
; APPLICANT: MUSHAWAR, ISA K.
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E
; HEPATITIS REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 539
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES
; STREET: ONE HUNDRED ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,185C
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 454:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-344-185C-454

Query Match 65.2%; Score 15; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
DB 4 LW 5

RESULT 28
US-08-424-550A-228
; Sequence 228, Application US/08424550A
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550A-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
DB 3 LW 4

RESULT 29
US-08-424-550B-228

```

; Sequence 228, Application US/08424550B
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 3 LW 4

RESULT 30
US-08-432-147-47
; Sequence 47, Application US/08432147
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Arondel, Vincent J.
; APPLICANT: Gibson, Susan I.
; APPLICANT: Somerville, Christopher R.
; TITLE OF INVENTION: Altered Linolenic and Linoleic Acid
; TITLE OF INVENTION: Content in Plants
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lawrence M. Lavin, Jr., Monsanto Co., B94F
; STREET: 700 Chesterfield Parkway North
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA

```

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; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,147
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCTUS94/01321
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA: EP 94908724.1
; FILING DATE: 04-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavin Jr., Lawrence M.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: 38-21(10650)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6670
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-432-147-47

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 3 LW 4

RESULT 31
US-08-467-344A-228
; Sequence 228, Application US/08467344A
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>

```


; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-467-344A-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
DB 3 LW 4

RESULT 32
US-08-486-749-228
; Sequence 228, Application US/08486749
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,749
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-749-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
DB 3 LW 4

RESULT 33
US-08-488-445A-228
; Sequence 228, Application US/08488445A
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,445A
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-445A-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 4 LW 5
||
DB 3 LW 4

RESULT 34
US-08-488-446-228

```
; Sequence 228, Application US/08488446
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-446-228

Query Match 65.2%; Score 15; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 3 LW 4

RESULT 35
US-08-530-325-14
; Sequence 14, Application US/08530325
; GENERAL INFORMATION:
; APPLICANT: HILGER, CHRISTOPH-STEPH
; APPLICANT: DINKELBOG, LUDGER
; APPLICANT: KRAMP, WOLFGANG
; APPLICANT: SCHIER, HANS-MARTIN
; TITLE OF INVENTION: CHELATING AGENTS OF THE TYPE XN1S1O1 FOR RADIOACTIVE I
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY
; STREET: Four Embarcadero Center, Suite 400
; CITY: San Francisco
; STATE: CA
```

```
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,325
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE94/00371
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: P 43 11 023.1
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dubb, Hubert E
; REGISTRATION NUMBER: 25,329
; REFERENCE/DOCKET NUMBER: WBLT 2005 (WO) PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-362-3800
; TELEFAX: 415-362-2928
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-530-325-14

Query Match 65.2%; Score 15; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 4 LW 5

RESULT 36
US-08-530-327-14
; Sequence 14, Application US/08530327
; GENERAL INFORMATION:
; APPLICANT: ERBER, SEBASTIAN
; APPLICANT: DINKELBOG, LUDGER
; APPLICANT: ROHLFS, GERHARD
; APPLICANT: SCHULTZE, PAUL-EBERHARD
; APPLICANT: NOLL, BERNHARD
; TITLE OF INVENTION: BIFUNCTIONAL CHELATORS AND THEIR USE IN RADIOPHARMACI
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY
; STREET: Four Embarcadero Center, Suite 400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,327
; FILING DATE:
; CLASSIFICATION: 424
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/DE94/00369
;; FILING DATE: 29-MAR-1994
;; APPLICATION NUMBER: P 43 11 021.5
;; FILING DATE: 31-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dubb, Hubert E
;; REGISTRATION NUMBER: 25,329
;; REFERENCE/DOCKET NUMBER: WBLT 2007 (WO) PA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-362-3800
;; TELEFAX: 415-362-2928
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
US-08-530-327-14

Query Match 65.2%; Score 15; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
DB 4 LW 5

RESULT 37
US-08-981-122-15
; Sequence 15, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide
; OTHER INFORMATION: synthesizing system (RaMPS)
US-08-981-122-15

Query Match 65.2%; Score 15; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
DB 1 LW 2

RESULT 38
US-08-981-122-38
; Sequence 38, Application US/08981122A

;; GENERAL INFORMATION:
;; APPLICANT: Hatanaka, Yoshihiro
;; APPLICANT: Aritomi, Masaharu
;; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/08/981,122A
;; CURRENT FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: JP 7-176904
;; EARLIER FILING DATE: 1995-06-21
;; EARLIER APPLICATION NUMBER: PCT/JP96/01734
;; EARLIER FILING DATE: 1996-06-21
;; NUMBER OF SEQ ID NOS: 90
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 38
;; LENGTH: 5
;; TYPE: PPT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: AMIDATION
;; LOCATION: 5
;; FEATURE:
;; OTHER INFORMATION: Sequence of a peptide synthesized in Examples 11 and 12 from L-form
;; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
;; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-38

Query Match 65.2%; Score 15; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
DB 4 LW 5

RESULT 39
US-08-981-122-43
; Sequence 43, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 5
; FEATURE:
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-43

Query Match 65.2%; Score 15; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
DB 4 LW 5

RESULT 40
US-08-981-122-51
; Sequence 51, Application US/08981122A
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122A
; CURRENT FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: JP 7-176904
; EARLIER FILING DATE: 1995-06-21
; EARLIER APPLICATION NUMBER: PCT/JP96/01734
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: AMIDATION
; LOCATION: 5
; FEATURE:
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
; OTHER INFORMATION: Fmoc amino acids by solid phase method using an automatic peptide
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-51

Query Match 65.2%; Score 15; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 41
US-09-209-676-30
; Sequence 30, Application US/09209676
; GENERAL INFORMATION:
; APPLICANT: Pangene Corporation
; TITLE OF INVENTION: The Use of Consensus Sequences for Targeted Homologous
; FILE REFERENCE: Gene Isolation and Recombination in Gene Families
; FILE REFERENCE: A-65678-1/RFT/NBC
; CURRENT APPLICATION NUMBER: US/09/209,676
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/070,734
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-209-676-30

Query Match 65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 42
US-09-284-327-1
; Sequence 1, Application US/09284327

; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding
; TITLE OF INVENTION: Such Enzymes and Methods for Producing Such Enzymes
; FILE REFERENCE: GC516-2-PCT
; CURRENT APPLICATION NUMBER: US/09/284,327
; CURRENT FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-284-327-1

Query Match 65.2%; Score 15; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 43
US-09-308-823A-582
; Sequence 582, Application US/09308823A
; GENERAL INFORMATION:
; APPLICANT: Warren, Richard
; TITLE OF INVENTION: Novel Prokaryotic Polynucleotides,
; TITLE OF INVENTION: Polypeptides and Their Uses
; FILE REFERENCE: P50596
; CURRENT APPLICATION NUMBER: US/09/308,823A
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 661
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 582
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-308-823A-582

Query Match 65.2%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 44
US-09-350-641-791
; Sequence 791, Application US/09350641
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1589
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791

```
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641-791

Query Match      65.2%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 1 LW 2

RESULT 45
US-09-350-641B-791
; Sequence 791, Application US/09350641B
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641B
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641B-791

Query Match      65.2%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 1 LW 2

RESULT 46
US-09-350-641C-791
; Sequence 791, Application US/09350641C
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-791

Query Match      65.2%; Score 15; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 1 LW 2

RESULT 47
US-09-410-568-9
; Sequence 9, Application US/09410568
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410,568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-410-568-9

Query Match      65.2%; Score 15; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 3 LW 4

RESULT 48
US-09-426-571-9
; Sequence 9, Application US/09426571
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 469C3
; CURRENT APPLICATION NUMBER: US/09/426,571
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
```

US-09-426-571-9

Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 3 LW 4

RESULT 49

US-09-454-684-9
 ; Sequence 9, Application US/09454684
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C4
 ; CURRENT APPLICATION NUMBER: US/09/454,684
 ; PRIOR FILING DATE: 1999-12-03
 ; NUMBER OF SEQ ID NOS: 303
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 9
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Chlamydia trachomatis
 ; ORGANISM: Chlamydia trachomatis

Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 3 LW 4

RESULT 50

US-09-454-684A-9
 ; Sequence 9, Application US/09454684A
 ; GENERAL INFORMATION:
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C4
 ; CURRENT APPLICATION NUMBER: US/09/454,684A
 ; PRIOR FILING DATE: 1999-12-03
 ; NUMBER OF SEQ ID NOS: 310
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 9
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Chlamydia trachomatis
 ; ORGANISM: Chlamydia trachomatis

Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 3 LW 4

RESULT 51

US-09-457-198A-25
 ; Sequence 25, Application US/09457198A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hartnett, James R.
 ; APPLICANT: Christine, Andrews A.
 ; TITLE OF INVENTION: Thermostable Enzyme for Nucleic Acid Detection
 ; FILE REFERENCE: Thermostable/nucleic acid detection
 ; CURRENT APPLICATION NUMBER: US/09/457,198A
 ; CURRENT FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 09/358,972
 ; PRIOR FILING DATE: 1999-07-21
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 25
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Pyrococcus furiosus
 ; ORGANISM: Pyrococcus furiosus

Query Match 65.2%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 4 LW 5

RESULT 52

US-09-515-965-791
 ; Sequence 791, Application US/09515965
 ; GENERAL INFORMATION:
 ; APPLICANT: Antczak, J.
 ; APPLICANT: Delmedico, M.
 ; APPLICANT: Erickson, J.
 ; APPLICANT: Lambert, D.
 ; APPLICANT: Sista, P.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
 ; FILE REFERENCE: 7872-073
 ; CURRENT APPLICATION NUMBER: US/09/515,965
 ; CURRENT FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 09/315,304
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1589
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 791
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 ; OTHER INFORMATION: Core polypeptide

Query Match 65.2%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 1 LW 2

RESULT 53

US-09-515-965A-791
 ; Sequence 791, Application US/09515965A
 ; GENERAL INFORMATION:
 ; APPLICANT: Antczak, J.
 ; APPLICANT: Delmedico, M.
 ; APPLICANT: Erickson, J.

; APPLICANT: Lambert, D.
 ; APPLICANT: Sista, P.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
 ; FILE REFERENCE: 7872-073
 ; CURRENT APPLICATION NUMBER: US/09/515,965A
 ; CURRENT FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 09/315,304
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1994
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 791
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 US-09-515-965A-791

Query Match 65.2%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 ||
 Db 1 LW 2

RESULT 54

US-09-515-965A-1657
 ; Sequence 1657, Application US/09515965A
 ; GENERAL INFORMATION:
 ; APPLICANT: Antczak, J.
 ; APPLICANT: Delmedico, M.
 ; APPLICANT: Erickson, J.
 ; APPLICANT: Lambert, D.
 ; APPLICANT: Sista, P.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
 ; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
 ; FILE REFERENCE: 7872-073
 ; CURRENT APPLICATION NUMBER: US/09/515,965A
 ; CURRENT FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 09/315,304
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: 09/082,279
 ; PRIOR FILING DATE: 1998-05-20
 ; NUMBER OF SEQ ID NOS: 1994
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1657
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Core polypeptide
 US-09-515-965A-1657

Query Match 65.2%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 ||
 Db 1 LW 2

RESULT 55

US-09-536-998-1
 ; Sequence 1, Application US/09536998
 ; GENERAL INFORMATION:
 ; APPLICANT: Bini, Alessandra

; APPLICANT: Kudryk, Bohdan
 ; TITLE OF INVENTION: MONOSPECIFIC ANTIBODY REACTIVE WITH MATRIXMETALLOPROTEINASE CLEAV
 ; FILE REFERENCE: 454-16CIP
 ; CURRENT APPLICATION NUMBER: US/09/536,998
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 08/900,895
 ; PRIOR FILING DATE: 1997-07-25
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-536-998-1

Query Match 65.2%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 ||
 Db 2 LW 3

RESULT 56

US-09-598-419-9
 ; Sequence 9, Application US/09598419
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Scholler, John
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C6
 ; CURRENT APPLICATION NUMBER: US/09/598,419
 ; CURRENT FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 357
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 9
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Chlamydia trachomatis
 US-09-598-419-9

Query Match 65.2%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.2e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 ||
 Db 3 LW 4

RESULT 57

US-09-632-426-30
 ; Sequence 30, Application US/09632426
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitchinson, Colin
 ; APPLICANT: Ropp, Traci M.
 ; APPLICANT: Swanson, Barbara A.
 ; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
 ; TITLE OF INVENTION: Compositions
 ; FILE REFERENCE: GCG30
 ; CURRENT APPLICATION NUMBER: US/09/632,426
 ; CURRENT FILING DATE: 2000-08-04
 ; NUMBER OF SEQ ID NOS: 86
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 30
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Box1

```

; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Asn or Gln
US-09-632-426-30

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 58
US-09-632-570-30
; Sequence 30, Application US/09632570
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Asn or Gln
; OTHER INFORMATION: BOX1
US-09-632-570-30

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 59
US-09-636-243A-75
; Sequence 75, Application US/09636243A
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243A-75

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 60
US-09-642-234-75
; Sequence 75, Application US/09642234
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004.20 / M4-US2
; CURRENT APPLICATION NUMBER: US/09/642,234
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-642-234-75

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

RESULT 61
US-09-657-276-723
; Sequence 723, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibadeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 723
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-723

Query Match      65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
   ||
Db 3 LW 4

```


Best Local Similarity 100.0%; Pred. No. 4.2e+06; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 62

US-09-657-276-724
; Sequence 724, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 724
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-724

Query Match 65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 63

US-09-657-276-734
; Sequence 734, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 734
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-734

Query Match 65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 64

US-09-657-276-1560
; Sequence 1560, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1560
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1560

Query Match 65.2%; Score 15; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 2 LW 3

RESULT 65

US-09-762-270-19
; Sequence 19, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOEREELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHIAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270

; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-19

Query Match 65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 66
US-09-762-270-20
; Sequence 21, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-20

Query Match 65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 67
US-09-762-270-21
; Sequence 21, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-21

Query Match 65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 68
US-09-762-270-22
; Sequence 22, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-22

Query Match 65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 69
US-09-762-270-23
; Sequence 23, Application US/09762270
; GENERAL INFORMATION:
; APPLICANT: DEPLA, ERIK
; APPLICANT: MOERRELS, HENRI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: BENZODIAZEPINES AND BENZOTHAZEPINES DERIVATIVES AND
; TITLE OF INVENTION: HBSAG PEPTIDES BINDING TO ANNEXINS, THEIR COMPOSITIONS
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 2551-54
; CURRENT APPLICATION NUMBER: US/09/762,270
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: PCT/EP99/06231

; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: EP 98870186.8
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: EP 99870062.9
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-762-270-23

Query Match 65.2%; Score 15; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 70

US-09-834-784-791
; Sequence 791, Application US/09834784
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-791

Query Match 65.2%; Score 15; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 1 LW 2

RESULT 71

US-09-841-132-9
; Sequence 9, Application US/09841132
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 9
; LENGTH: 5

; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-9

Query Match 65.2%; Score 15; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 72

US-09-920-306-21
; Sequence 21, Application US/09920306
; GENERAL INFORMATION:
; APPLICANT: Unilever PLC
; APPLICANT: Unilever NV
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for
; FILE REFERENCE: Hormonal Analyses
; CURRENT APPLICATION NUMBER: US/09/920,306
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: EP00306613.1
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-920-306-21

Query Match 65.2%; Score 15; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 2 LW 3

RESULT 73

US-09-350-369C-513
; Sequence 513, Application US/09350369C
; GENERAL INFORMATION:
; APPLICANT: Samuel E. Hopkins
; APPLICANT: Elizabeth M. Dimassimo
; APPLICANT: Pamela P. Ruskak
; APPLICANT: Thomas Michael Venetta
; TITLE OF INVENTION: Methods and Compositions for Detection of HIV GP41 Peptides
; FILE REFERENCE: 7872-068-999
; CURRENT APPLICATION NUMBER: US/09/350,369C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1 (HIV-1)
US-09-350-369C-513

Query Match 65.2%; Score 15; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||

Db 1 LW 2

RESULT 74

US-09-350-369C-1389
; Sequence 1389, Application US/09350369C
; GENERAL INFORMATION:
; APPLICANT: Samuel E. Hopkins
; APPLICANT: Elizabeth M. Dimassimo
; APPLICANT: Pamela P. Rusnak
; APPLICANT: Thomas Michael Venetta
; TITLE OF INVENTION: Methods and Compositions for Detection of HIV GP41 Peptides and H
; TITLE OF INVENTION: GP41-Like Peptides
; FILE REFERENCE: 7872-068-999
; CURRENT APPLICATION NUMBER: US/09/350,369C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1389
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus-1 (HIV-1)
US-09-350-369C-1389

Query Match 65.2%; Score 15; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 1 LW 2

RESULT 75

US-10-005-305-36
; Sequence 36, Application US/10005305
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-36

Query Match 65.2%; Score 15; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 1 LW 2

Search completed: February 12, 2003, 10:55:29
Job time: 133 secs

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OM protein - protein search, using sw model

Run on: February 12, 2003, 10:51:59 ; Search time 18 Seconds
(without alignments)
23.274 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 1873

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep: *
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep: *
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	82.6	5	5	US-09-281-717A-3
2	15	65.2	5	5	US-09-636-243B-75
3	13	56.5	5	5	US-09-968-744A-211
4	13	56.5	5	5	US-09-968-744A-217
5	13	56.5	5	6	US-10-174-717A-51
6	13	56.5	5	6	US-10-099-056-2683
7	12	52.2	5	6	US-10-174-717A-94
8	12	52.2	5	6	US-10-053-498B-320
9	11	47.8	5	1	PCT-US02-32657-65
10	11	47.8	5	1	PCT-US02-33556-34
11	11	47.8	5	1	PCT-US02-33556-36
12	11	47.8	5	1	PCT-US02-33556-40
13	11	47.8	5	1	PCT-US02-33985-2
14	11	47.8	5	1	PCT-US02-34760-21
15	11	47.8	5	1	PCT-US02-34760-46
16	11	47.8	5	1	PCT-US02-34760-47
17	11	47.8	5	1	PCT-US02-35606-2
18	11	47.8	5	1	PCT-US02-16525A-26
19	11	47.8	5	1	PCT-US02-24469-21
20	11	47.8	5	1	PCT-US02-24310-166
21	11	47.8	5	1	PCT-US02-24469A-21
22	11	47.8	5	1	PCT-US02-39109-15
23	11	47.8	5	1	PCT-US02-32307-23
24	11	47.8	5	1	PCT-US02-39643-5
25	11	47.8	5	1	PCT-US02-40891-1113
26	11	47.8	5	1	PCT-US02-40892-398
27	11	47.8	5	1	PCT-US02-33835-61
28	11	47.8	5	1	PCT-US03-00440-14
29	11	47.8	5	1	PCT-US03-00440-26
30	11	47.8	5	1	PCT-US03-00440-38
31	11	47.8	5	4	US-08-832-443C-13
32	11	47.8	5	4	US-08-908-416B-147
33	11	47.8	5	4	US-08-908-416B-152
34	11	47.8	5	4	US-08-908-416B-157
35	11	47.8	5	4	US-08-908-416B-162
36	11	47.8	5	4	US-08-908-416B-167
37	11	47.8	5	4	US-08-908-416B-172
38	11	47.8	5	5	US-09-721-456-540
39	11	47.8	5	5	US-09-533-800-16
40	11	47.8	5	5	US-09-813-484-1
41	11	47.8	5	5	US-09-726-348B-5
42	11	47.8	5	5	US-09-653-812B-145
43	11	47.8	5	5	US-09-653-812B-152
44	11	47.8	5	5	US-09-556-972-12
45	11	47.8	5	5	US-09-610-650B-18
46	11	47.8	5	5	US-09-943-120-1
47	11	47.8	5	5	US-09-936-759-32
48	11	47.8	5	5	US-09-969-748C-19
49	11	47.8	5	5	US-09-969-748C-20
50	11	47.8	5	5	US-09-553-800D-16
51	11	47.8	5	5	US-09-720-278A-1
52	11	47.8	5	5	US-09-720-278A-2
53	11	47.8	5	5	US-09-720-278A-3
54	11	47.8	5	5	US-09-720-278A-5
55	11	47.8	5	5	US-09-720-278A-21
56	11	47.8	5	5	US-09-720-278A-23
57	11	47.8	5	5	US-09-720-278A-27
58	11	47.8	5	5	US-09-636-243B-30
59	11	47.8	5	5	US-09-636-243B-35
60	11	47.8	5	5	US-09-636-243B-44
61	11	47.8	5	5	US-09-636-243B-56
62	11	47.8	5	5	US-09-636-243B-57
63	11	47.8	5	5	US-09-636-243B-58
64	11	47.8	5	5	US-09-636-243B-59
65	11	47.8	5	5	US-09-636-243B-60
66	11	47.8	5	5	US-09-636-243B-61
67	11	47.8	5	5	US-09-636-243B-62
68	11	47.8	5	5	US-09-636-243B-63
69	11	47.8	5	5	US-09-636-243B-64
70	11	47.8	5	5	US-09-636-243B-76
71	11	47.8	5	5	US-09-636-243B-77
72	11	47.8	5	5	US-09-636-243B-78
73	11	47.8	5	5	US-09-254-180C-1
74	11	47.8	5	5	US-09-676-475A-278
75	11	47.8	5	5	US-09-920-262A-1
76	11	47.8	5	5	US-09-910-505B-27
77	11	47.8	5	6	US-10-245-475-12
78	11	47.8	5	6	US-10-264-237-2
79	11	47.8	5	6	US-10-266-829-2
80	11	47.8	5	6	US-10-281-102-14
81	11	47.8	5	6	US-10-269-695-65
82	11	47.8	5	6	US-10-272-147-12
83	11	47.8	5	6	US-10-198-069-21
84	11	47.8	5	6	US-10-198-070-10
85	11	47.8	5	6	US-10-209-582-2
86	11	47.8	5	6	US-10-069-605-111
87	11	47.8	5	6	US-10-069-605-112
88	11	47.8	5	6	US-10-069-605-115
89	11	47.8	5	6	US-10-264-634-8
90	11	47.8	5	6	US-10-283-549-21
91	11	47.8	5	6	US-10-283-549-46
92	11	47.8	5	6	US-10-283-549-47
93	11	47.8	5	6	US-10-277-802-2
94	11	47.8	5	6	US-10-174-368A-14
95	11	47.8	5	6	US-10-218-253-6
96	11	47.8	5	6	US-10-306-885-12
97	11	47.8	5	6	US-10-313-135-11
98	11	47.8	5	6	US-10-226-795-23
99	11	47.8	5	6	US-10-058-513-33
100	11	47.8	5	6	US-10-058-513-33

100 11 47.8 5 6 US-10-058-513-38

Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-281-717A-3
; Sequence 3, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun
; APPLICANT: Fletterick, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: COACTIVAOR BINDING
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281,717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/079,956
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Variant
; LOCATION: (2)..(3)
; OTHER INFORMATION: Xaa is any amino acid

US-09-281-717A-3

Query Match 82.6%; Score 19; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXLW 5
|||
Db 1 FXLW 5

RESULT 2
US-09-636-243B-75
; Sequence 75, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence

US-09-636-243B-75
Query Match 65.2%; Score 15; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 3
US-09-968-744A-211
; Sequence 211, Application US/09968744A
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 211
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-211

Query Match 56.5%; Score 13; DB 5; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 4 MW 5

RESULT 4
US-09-968-744A-217
; Sequence 217, Application US/09968744A
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-217

Query Match 56.5%; Score 13; DB 5; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 4 MW 5

RESULT 5

US-10-174-717A-51
; Sequence 51, Application US/10174717A
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, St. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSeq Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-10-174-717A-51

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 2 MW 3

RESULT 6

US-10-099-056-2683
; Sequence 2683, Application US/10099056
; GENERAL INFORMATION:
; APPLICANT: Hybrigenics
; APPLICANT: Pierre Legrain
; TITLE OF INVENTION: More and more protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4838A
; CURRENT APPLICATION NUMBER: US/10/099,056
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 60/275,734

; PRIOR FILING DATE: 2001/03/14
; NUMBER OF SEQ ID NOS: 2850
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2683
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Translation of SEQ ID NO:691
US-10-099-056-2683

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 1 IW 2

RESULT 7

US-10-174-717A-94
; Sequence 94, Application US/10174717A
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, St. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSeq Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-10-174-717A-94

Query Match 52.2%; Score 12; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|

Db 2 VW 3

RESULT 8

US-10-053-498B-320
; Sequence 320, Application US/10053498B
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Querfelli, Quathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 320
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Random peptide in coliphage M13
US-10-053-498B-320

Query Match 52.2%; Score 12; DB 6; Length 5;
Best Local Similarity 40.0%; Pred. No. 3.5e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FHWVW 5

RESULT 9

PCT-US02-32657-65
; Sequence 65, Application PC/TUS0232657
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
; FILE REFERENCE: A-801B
; CURRENT APPLICATION NUMBER: PCT/US02/32657
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 60/414,155
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328,624
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide capable of binding to Ang-2
PCT-US02-32657-65

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 10

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;

PCT-US02-33556-34
; Sequence 34, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-34

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 4 W 4

RESULT 11

PCT-US02-33556-36
; Sequence 36, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-36

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 4 W 4

RESULT 12

PCT-US02-33556-40
; Sequence 40, Application PC/TUS0233556
; GENERAL INFORMATION:
; APPLICANT: Amgen, Inc.
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: PCT/US02/33556
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-33556-40

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 4 W 4

RESULT 13

PCT-US02-33985-2
; Sequence 21, Application PC/TUS0233985
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 16 Human Secreted Proteins
; FILE REFERENCE: PS739PCT
; CURRENT APPLICATION NUMBER: PCT/US02/33985
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/330,629
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
PCT-US02-33985-2

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 14

PCT-US02-34760-21
; Sequence 21, Application PC/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Haviv, Fortuna
; APPLICANT: Bradley, Michael F.
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
; FILE REFERENCE: 6854.WO.01
; CURRENT APPLICATION NUMBER: PCT/US02/34760
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 10/263,811
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 10/000,540
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/000,007
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antiangiogenic Peptide
; NAME/KEY: VARIANT
; LOCATION: (2)...(2)
; OTHER INFORMATION: Xaa = Nva at position 2
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa = prolylethylamide at position 5

PCT-US02-34760-21

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 15

PCT-US02-34760-46
; Sequence 46, Application PC/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Haviv, Fortuna
; APPLICANT: Bradley, Michael F.
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
; FILE REFERENCE: 6854.WO.01
; CURRENT APPLICATION NUMBER: PCT/US02/34760
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 10/263,811
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 10/000,540
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/000,007
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antiangiogenic Peptide
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-46

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 2 W 2

RESULT 16

PCT-US02-34760-47
; Sequence 47, Application PC/TUS0234760
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Haviv, Fortuna
; APPLICANT: Bradley, Michael F.
; TITLE OF INVENTION: TETRA-, PENTA-, HEXA- AND HEPTAPEPTIDES
; FILE REFERENCE: 6854.WO.01
; CURRENT APPLICATION NUMBER: PCT/US02/34760
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 10/263,811
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 10/000,540
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/000,007
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47

```

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antiangiogenic Peptide
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa = proethylamide at position 5
PCT-US02-34760-47

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      2 W 2

RESULT 17
PCT-US02-35606-2
; Sequence 2, Application PC/TUS0235606
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 41 Human Secreted Proteins
; FILE REFERENCE: PS740PCT
; CURRENT APPLICATION NUMBER: PCT/US02/35606
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/331,046
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Site
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
PCT-US02-35606-2

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 18
PCT-US02-16525A-26
; Sequence 26, Application PC/TUS0216525A
; GENERAL INFORMATION:
; APPLICANT: Bell et al.
; TITLE OF INVENTION: Chemokine Beta-1 Fusion Proteins
; FILE REFERENCE: PF556PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16525A
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,212
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

```

```

PCT-US02-16525A-26

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      1 W 1

RESULT 19
PCT-US02-24469-21
; Sequence 21, Application PC/TUS0224469
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 20900Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469-21

Query Match          47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
Db      3 W 3

RESULT 20
PCT-US02-24310-166
; Sequence 166, Application PC/TUS0224310
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: PCT/US02/24310
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: thioesterase motif
PCT-US02-24310-1166

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 2 W 2

RESULT 21

PCT-US02-24469A-21
; Sequence 21, Application PC/TUS0224469A
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: Biological Assay Detection Method
; FILE REFERENCE: PCT 20900Y
; CURRENT APPLICATION NUMBER: PCT/US02/24469A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/310,599
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa is a variable which may be
; OTHER INFORMATION: A,R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(5)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-24469A-21

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 3 W 3

RESULT 22

PCT-US02-39109-15
; Sequence 15, Application PC/TUS0239109
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; APPLICANT: Ruscetti, Francis W.
; APPLICANT: Ruff, Michael R.
; TITLE OF INVENTION: PEPTIDE T STIMULATES CTL RESPONSES
; FILE REFERENCE: 14014.0404P1
; CURRENT APPLICATION NUMBER: PCT/US02/39109
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/338,971
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
PCT-US02-39109-15

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 3 W 3

RESULT 23

PCT-US02-32307-23
; Sequence 23, Application PC/TUS0232307
; GENERAL INFORMATION:
; APPLICANT: IMMUNOMEDICS, INC.
; TITLE OF INVENTION: COMBINATION THERAPY WITH CLASS III ANTI-CEA MONOCLONAL ANTIBODIES
; FILE REFERENCE: 018733-1148
; CURRENT APPLICATION NUMBER: PCT/US02/32307
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
PCT-US02-32307-23

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 3 W 3

RESULT 24

PCT-US02-39643-5
; Sequence 5, Application PC/TUS0239643
; GENERAL INFORMATION:
; APPLICANT: Smith, Thomas M
; APPLICANT: Kirtley, Terence L
; TITLE OF INVENTION: APYRASE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 0091830/0502531
; CURRENT APPLICATION NUMBER: PCT/US02/39643
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-39643-5

Query Match 47.8%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 2 W 2

RESULT 25

PCT-US02-40891-1113
; Sequence 1113, Application PC/TUS0240891
; GENERAL INFORMATION:

; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/431684
 ; PRIOR FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US03-00440-14

Query Match 47.8%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 3 W 3

RESULT 29
 PCT-US03-00440-26
 ; Sequence 26, Application PC/TUS0300440
 ; GENERAL INFORMATION:
 ; APPLICANT: Medarex, Inc. et al.
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
 ; FILE REFERENCE: MXI-180PC
 ; CURRENT APPLICATION NUMBER: PCT/US03/00440
 ; CURRENT FILING DATE: 2003-01-07
 ; PRIOR APPLICATION NUMBER: US 60/347649
 ; PRIOR FILING DATE: 2002-01-09
 ; PRIOR APPLICATION NUMBER: US 60/404427
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/431684
 ; PRIOR FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US03-00440-26

Query Match 47.8%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 4 W 4

RESULT 30
 PCT-US03-00440-38
 ; Sequence 38, Application PC/TUS0300440
 ; GENERAL INFORMATION:
 ; APPLICANT: Medarex, Inc. et al.
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
 ; FILE REFERENCE: MXI-180PC
 ; CURRENT APPLICATION NUMBER: PCT/US03/00440
 ; CURRENT FILING DATE: 2003-01-07
 ; PRIOR APPLICATION NUMBER: US 60/347649
 ; PRIOR FILING DATE: 2002-01-09
 ; PRIOR APPLICATION NUMBER: US 60/404427
 ; PRIOR FILING DATE: 2002-08-19
 ; PRIOR APPLICATION NUMBER: US 60/431684
 ; PRIOR FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 38
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

PCT-US03-00440-38

Query Match 47.8%; Score 11; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 4 W 4

RESULT 31
 US-08-832-443C-13
 ; Sequence 13, Application US/08832443C
 ; GENERAL INFORMATION:
 ; APPLICANT: TSYRLOVA, IRENA
 ; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
 ; USES THEREOF
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHVE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ; CITY: ARLINGTON
 ; STATE: VIRGINIA
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/832,443C
 ; FILING DATE: 03-Apr-1997
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/627,173
 ; FILING DATE: 03-APR-1996
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-08-832-443C-13

Query Match 47.8%; Score 11; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
 |
 Db 3 W 3

RESULT 32
 US-08-908-416B-147
 ; Sequence 147, Application US/08908416B
 ; GENERAL INFORMATION:
 ; APPLICANT: JONCZYK, ALFRED
 ; APPLICANT: GOODMAN, SIMON
 ; APPLICANT: DIEFENBACH, BEATE
 ; APPLICANT: KESSLER, HORST
 ; TITLE OF INVENTION: BIOTIN DERIVATIVES
 ; FILE REFERENCE: MERCK-1851
 ; CURRENT APPLICATION NUMBER: US/08/908,416B
 ; CURRENT FILING DATE: 1997-08-07
 ; PRIOR APPLICATION NUMBER: 08/710,251
 ; PRIOR FILING DATE: 1996-09-13

```
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-08-908-416B-147

Query Match          47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 33
US-08-908-416B-152
; Sequence 152, Application US/08908416B
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: GOODMAN, SIMON
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: KESSLER, HORST
; APPLICANT: FINSINGER, DIRK
; TITLE OF INVENTION: BIOTIN DERIVATIVES
; FILE REFERENCE: MERCK-1851
; CURRENT APPLICATION NUMBER: US/08/908,416B
; PRIOR FILING DATE: 1997-08-07
; PRIOR APPLICATION NUMBER: 08/710,251
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 152
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-08-908-416B-152

Query Match          47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 34
US-08-908-416B-157
; Sequence 157, Application US/08908416B
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: GOODMAN, SIMON
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: KESSLER, HORST
; APPLICANT: FINSINGER, DIRK
; TITLE OF INVENTION: BIOTIN DERIVATIVES
; FILE REFERENCE: MERCK-1851
; CURRENT APPLICATION NUMBER: US/08/908,416B
; PRIOR FILING DATE: 1997-08-07
; PRIOR APPLICATION NUMBER: 08/710,251
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-08-908-416B-157

Query Match          47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 35
US-08-908-416B-162
; Sequence 162, Application US/08908416B
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: GOODMAN, SIMON
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: KESSLER, HORST
; APPLICANT: FINSINGER, DIRK
; TITLE OF INVENTION: BIOTIN DERIVATIVES
; FILE REFERENCE: MERCK-1851
; CURRENT APPLICATION NUMBER: US/08/908,416B
; PRIOR FILING DATE: 1997-08-07
; PRIOR APPLICATION NUMBER: 08/710,251
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 162
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-08-908-416B-162

Query Match          47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 W 5
      |
Db      1 W 1

RESULT 36
US-08-908-416B-167
; Sequence 167, Application US/08908416B
; GENERAL INFORMATION:
; APPLICANT: JONCZYK, ALFRED
; APPLICANT: GOODMAN, SIMON
; APPLICANT: DIEFENBACH, BEATE
; APPLICANT: KESSLER, HORST
; APPLICANT: FINSINGER, DIRK
; TITLE OF INVENTION: BIOTIN DERIVATIVES
; FILE REFERENCE: MERCK-1851
; CURRENT APPLICATION NUMBER: US/08/908,416B
; PRIOR FILING DATE: 1997-08-07
; PRIOR APPLICATION NUMBER: 08/710,251
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 167
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-08-908-416B-167
```

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-908-416B-167

Query Match 47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 37

US-08-908-416B-172
Sequence 172, Application US/08908416B
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: GOODMAN, SIMON
APPLICANT: DIEFENBACH, BEATE
APPLICANT: KESSLER, HORST
APPLICANT: FINSINGER, DIRK
TITLE OF INVENTION: BIOTIN DERIVATIVES
FILE REFERENCE: MERCK-1851
CURRENT APPLICATION NUMBER: US/08/908.416B
CURRENT FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 08/710,251
PRIOR FILING DATE: 1996-09-13
NUMBER OF SEQ ID NOS: 175
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 172
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-08-908-416B-172

Query Match 47.8%; Score 11; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 38

US-09-721-456-540
Sequence 540, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 540:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 540:
US-09-721-456-540

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 39

US-09-533-800-16
Sequence 16, Application US/09533800
GENERAL INFORMATION:
APPLICANT: Firestone, Raymond A.
APPLICANT: Rettig, Wolfgang J.
APPLICANT: Lenter, Martin U.
APPLICANT: Peters, Stefan
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Mack, Juergen
APPLICANT: Leipert, Dietmar
APPLICANT: Park, John E.
APPLICANT: Telan, Leila A.
TITLE OF INVENTION: FAP-Activated Anti-Tumour Compounds
FILE REFERENCE: 1/1087 US
CURRENT APPLICATION NUMBER: US/09/533,800
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/134,136
PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Precursor
 US-09-533-800-16

Query Match 47.8%; Score 11; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 4 W 4

RESULT 40

US-09-813-484-1
 ; Sequence 1, Application US/09813484

; GENERAL INFORMATION:
 ; APPLICANT: Unger, Evan C.
 ; TITLE OF INVENTION: Novel Methods Of Ultrasound Treatment Using Gas Or Gaseous Precursor
 ; FILE REFERENCE: UN91600
 ; CURRENT APPLICATION NUMBER: US/09/813,484
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 08/929,847
 ; PRIOR FILING DATE: 1997-09-15
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Completely synthetic sequence
 ; NAME/KEY: misc feature
 ; LOCATION: (4)-(4)
 ; OTHER INFORMATION: Xaa is azetidine
 US-09-813-484-1

Query Match 47.8%; Score 11; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 41

US-09-726-348B-5
 ; Sequence 5, Application US/09726348B

; GENERAL INFORMATION:
 ; APPLICANT: Wei, Ying-Fei
 ; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII
 ; FILE REFERENCE: PF220P1
 ; CURRENT APPLICATION NUMBER: US/09/726,348B
 ; CURRENT FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: 08/778,545
 ; PRIOR FILING DATE: 1997-01-03
 ; PRIOR APPLICATION NUMBER: 60/011,136
 ; PRIOR FILING DATE: 1996-01-04
 ; PRIOR APPLICATION NUMBER: 60/168,387
 ; PRIOR FILING DATE: 1999-12-02
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5 ;

; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: WSXWS motif
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (3)..(3)
 ; OTHER INFORMATION: Xaa equals any amino acid
 US-09-726-348B-5

Query Match 47.8%; Score 11; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 1 W 1

RESULT 42

US-09-653-812B-145
 ; Sequence 145, Application US/09653812B

; GENERAL INFORMATION:
 ; APPLICANT: KAZAZIAN, HAIG H.
 ; APPLICANT: BOEKE, JEFF D.
 ; APPLICANT: MORAN, JOHN V.
 ; APPLICANT: BETH, DOMBROSKI A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
 ; FILE REFERENCE: 9596-23U3 (053893-5006-02)
 ; CURRENT APPLICATION NUMBER: US/09/653,812B
 ; CURRENT FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: US 08/847,844
 ; PRIOR FILING DATE: 1997-04-28
 ; PRIOR APPLICATION NUMBER: US 08/749,805
 ; PRIOR FILING DATE: 1996-11-15
 ; PRIOR APPLICATION NUMBER: US 60/006,831
 ; PRIOR FILING DATE: 1995-11-16
 ; NUMBER OF SEQ ID NOS: 152
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 145
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Wild type L1.2mneoI construct
 US-09-653-812B-145

Query Match 47.8%; Score 11; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
 |
 Db 2 W 2

RESULT 43

US-09-653-812B-152
 ; Sequence 152, Application US/09653812B

; GENERAL INFORMATION:
 ; APPLICANT: KAZAZIAN, HAIG H.
 ; APPLICANT: BOEKE, JEFF D.
 ; APPLICANT: MORAN, JOHN V.
 ; APPLICANT: BETH, DOMBROSKI A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
 ; FILE REFERENCE: 9596-23U3 (053893-5006-02)
 ; CURRENT APPLICATION NUMBER: US/09/653,812B
 ; CURRENT FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: US 08/847,844
 ; PRIOR FILING DATE: 1997-04-28
 ; PRIOR APPLICATION NUMBER: US 08/749,805
 ; PRIOR FILING DATE: 1996-11-15

;; PRIOR APPLICATION NUMBER: US 60/006,831
;; PRIOR FILING DATE: 1995-11-16
;; NUMBER OF SEQ ID NOS: 152
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 152
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Mutant L1.2mneoI construct
US-09-653-812B-152

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 2 W 2

RESULT 44
US-09-556-972-12
;; Sequence 12, Application US/09556972
;; GENERAL INFORMATION:
;; APPLICANT: TORIGOE, Kakuji
;; OKURA, Takamori
;; KURIMOTO, Musashi
;; TITLE OF INVENTION: POLYPEPTIDES
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 300
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/556,972
;; FILING DATE: 24-Apr-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/996,338
;; FILING DATE: 22-DEC-1997
;; APPLICATION NUMBER: JP 74,697/1997
;; FILING DATE: 12-MAR-1997
;; APPLICATION NUMBER: JP 215,488/1997
;; FILING DATE: 28-JUL-1997
;; APPLICATION NUMBER: JP 291,837/1997
;; FILING DATE: 09-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: TORIGOE=3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-556-972-12

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 W 5
|
Db 1 W 1

RESULT 45
US-09-610-650B-18
;; Sequence 18, Application US/09610650B
;; GENERAL INFORMATION:
;; APPLICANT: Olsen et al.
;; TITLE OF INVENTION: Human Frezzled-Like Protein
;; FILE REFERENCE: PF389C1
;; CURRENT APPLICATION NUMBER: US/09/610,650B
;; CURRENT FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: 09/132,315
;; PRIOR FILING DATE: 1998-08-11
;; PRIOR APPLICATION NUMBER: 60/055,715
;; PRIOR FILING DATE: 1997-08-12
;; PRIOR APPLICATION NUMBER: 60/081,438
;; PRIOR FILING DATE: 1998-04-10
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (3)..(3)
;; OTHER INFORMATION: Xaa is any amino acid
US-09-610-650B-18

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5
|
Db 1 W 1

RESULT 46
US-09-943-120-1
;; Sequence 1, Application US/09943120
;; GENERAL INFORMATION:
;; APPLICANT: Rothschild, Kenneth J.
;; Sonar, Sanjay M.
;; Olejnik, Jerzy
;; TITLE OF INVENTION: Methods for the Detection and Isolation
;; OF Proteins
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MEDLEN & CARROLL, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/943,120
;; FILING DATE: 30-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/307,579
;; FILING DATE: 07-May-1999
;; APPLICATION NUMBER: 08/884,325

; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: AMBER-03242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-943-120-1

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 47
US-09-936-759-32
; Sequence 32, Application US/09936759
; GENERAL INFORMATION:
; APPLICANT: JEFFERSON, RICHARD
; APPLICANT: MAYER, JORGE E.
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
; FILE REFERENCE: 076518-0150
; CURRENT APPLICATION NUMBER: US/09/936,759
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: PCT/US00/07107
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/270,957
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 09/149,927
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,263
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-936-759-32

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 48
US-09-969-748C-19
; Sequence 19, Application US/09969748C
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven

; APPLICANT: BASU, Amareesh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence conserved in pIgr protein
US-09-969-748C-19

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 2 W 2

RESULT 49
US-09-969-748C-20
; Sequence 20, Application US/09969748C
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Amareesh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amino acid sequence conserved in pIgr protein
US-09-969-748C-20

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|

Db 2" W 2

US-09-553-800D-16

RESULT 50

; Sequence 16, Application US/09553800D

; GENERAL INFORMATION:

; APPLICANT: Firestone, Raymond A.

; APPLICANT: Rettig, Wolfgang J.

; APPLICANT: Lenter, Martin U.

; APPLICANT: Peters, Stefan

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Mack, Juergen

; APPLICANT: Leipert, Dietmar

; APPLICANT: Park, John E.

; APPLICANT: Telan, Leila A.

; TITLE OF INVENTION: FAP-Activated Anti-Tumour Compounds

; FILE REFERENCE: 1/1087 US

; CURRENT APPLICATION NUMBER: US/09/553.800D

; CURRENT FILING DATE: 2000-04-21

; PRIOR APPLICATION NUMBER: US 60/134,136

; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 16

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Precursor

US-09-553-800D-16

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

US-09-720-278A-1

RESULT 51

; Sequence 1, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-1

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

US-09-720-278A-2

RESULT 52

; Sequence 2, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 2

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-2

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

US-09-720-278A-3

RESULT 53

; Sequence 3, Application US/09720278A

; GENERAL INFORMATION:

; APPLICANT: Swart, Pieter Jacob

; APPLICANT: Kuipers, Maria Elizabeth

; APPLICANT: Meijer, Dirk Klaas Fokke

; APPLICANT: Hageman, Robert Johan Joseph

; APPLICANT: Van Den Berg, Jeroen Johannes Maria

; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or

; FILE REFERENCE: 702-002214

; CURRENT APPLICATION NUMBER: US/09/720,278A

; CURRENT FILING DATE: 2001-05-24

; PRIOR APPLICATION NUMBER: PCT/EP99/04067

; PRIOR FILING DATE: 1999-06-28

; PRIOR APPLICATION NUMBER: EP 98203765.7

; PRIOR FILING DATE: 1998-11-06

; PRIOR APPLICATION NUMBER: NL 1010284

; PRIOR FILING DATE: 1998-10-09

; PRIOR APPLICATION NUMBER: NL 1009505

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: Microsoft Word 97 SR-2

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: polypeptide

US-09-720-278A-3

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

Db 4 W 4

```

; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-3

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      4 W 4

RESULT 54
US-09-720-278A-5
; Sequence 5, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-5

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      2 W 2

RESULT 55
US-09-720-278A-21
; Sequence 21, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24

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; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-21

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      3 W 3

RESULT 56
US-09-720-278A-23
; Sequence 23, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob
; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 23
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-23

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 W 5
      |
Db      3 W 3

RESULT 57
US-09-720-278A-27
; Sequence 27, Application US/09720278A
; GENERAL INFORMATION:
; APPLICANT: Swart, Pieter Jacob

```

; APPLICANT: Kuipers, Maria Elizabeth
; APPLICANT: Meijer, Dirk Klaas Fokke
; APPLICANT: Hageman, Robert Johan Joseph
; APPLICANT: Van Den Berg, Jeroen Johannes Maria
; TITLE OF INVENTION: Pharmaceutical preparations for use in combatting or
; TITLE OF INVENTION: Preventing surface infections caused by microorganisms
; FILE REFERENCE: 702-002214
; CURRENT APPLICATION NUMBER: US/09/720,278A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/EP99/04067
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: EP 98203765.7
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: NL 1010284
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: NL 1009505
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-720-278A-27

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 3 W 3

RESULT 58
US-09-636-243B-30
; Sequence 30, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-30

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 5 W 5

RESULT 59
US-09-636-243B-35
; Sequence 35, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.

; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-35

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 60
US-09-636-243B-44
; Sequence 44, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-44

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 1 W 1

RESULT 61
US-09-636-243B-56
; Sequence 56, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 56
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-56

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 62
US-09-636-243B-57
; Sequence 57, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-57

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 63
US-09-636-243B-58
; Sequence 58, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-58

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 64
US-09-636-243B-59
; Sequence 59, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-59

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3

RESULT 65
US-09-636-243B-60
; Sequence 60, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-60

Query Match          47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
Db 3 W 3
```

RESULT 66

US-09-636-243B-61
; Sequence 61, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-61

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

RESULT 67

US-09-636-243B-62
; Sequence 62, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-62

Query Match 47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

RESULT 68

US-09-636-243B-63
; Sequence 63, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B

; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-63

Query Match

47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 1 W 1

RESULT 69

US-09-636-243B-64
; Sequence 64, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-64

Query Match

47.8%; Score 11; DB 5; Length 5;

Best Local Similarity 100.0%; Pred. No. 3.5e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 W 5

DB 3 W 3

RESULT 70

US-09-636-243B-76
; Sequence 76, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; APPLICANT: PABO, Carl O.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-76

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 71
US-09-636-243B-77
; Sequence 77, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-77

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 72
US-09-636-243B-78
; Sequence 78, Application US/09636243B
; GENERAL INFORMATION:
; APPLICANT: WANG, Bryan S.
; TITLE OF INVENTION: DIMERIZING PEPTIDES
; FILE REFERENCE: 8325-1004 / M4-US1
; CURRENT APPLICATION NUMBER: US/09/636,243B
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/148,422
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequential
; OTHER INFORMATION: block reoptimization sequence
US-09-636-243B-78

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 4 W 4

RESULT 73
US-09-254-180C-1
; Sequence 1, Application US/09254180C
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-1

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|
Db 3 W 3

RESULT 74
US-09-676-475A-278
; Sequence 278, Application US/09676475A
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-278

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 W 5
|

Db 1 W 1

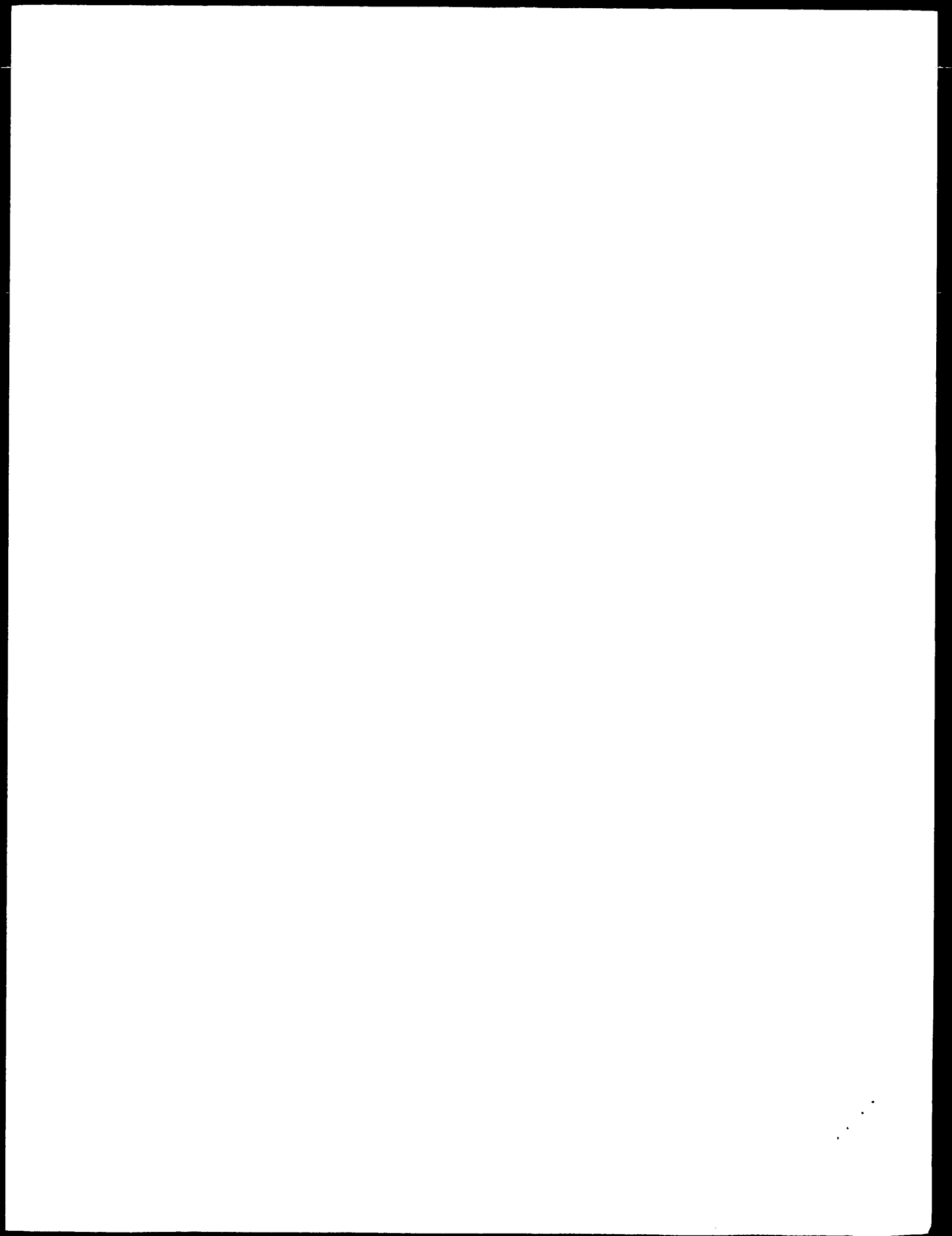
RESULT 75

US-09-920-262A-1
; Sequence 1, Application US/09920262A
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-1

Query Match 47.8%; Score 11; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. NO. 3.5e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 W 5
|
Db 3 W 3

Search completed: February 12, 2003, 10:55:52
Job time : 18 secs



ALIGNMENTS

RESULT 1
 US-08-424-957-4
 ; Sequence 4, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickseley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957
 ; FILING DATE: 19-APR-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WHd
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-424-957-4

Query Match 82.6%; Score 19; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 |||||
 Db 1 FXXLW 5

RESULT 2
 US-08-424-957-5
 ; Sequence 5, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickseley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco

Query Match 82.6%; Score 19; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 |||||
 Db 1 FXXLW 5

US-09-035-686-4
 ; Sequence 4, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickseley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957
 ; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.

Query Match 82.6%; Score 19; DB 1; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 |||||
 Db 1 FXELW 5

RESULT 3
 US-09-035-686-4
 ; Sequence 4, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickseley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957
 ; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-09-035-686-4

Query Match 82.6%; Score 19; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FXXLW 5
 |||||
 Db 1 FXXLW 5

RESULT 4

US-09-035-686-5
 ; Sequence 5, Application US/09035686
 ; Patent No. 6153391
 ; GENERAL INFORMATION:
 ; APPLICANT: Pickle, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/035,686
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/424,957
 ; FILING DATE: 19-APR-1995
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WHD
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-09-035-686-5

Query Match 82.6%; Score 19; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXLW 5
 |||||
 Db 1 FXXLW 5

RESULT 5

US-09-099-053-3
 ; Sequence 3, Application US/09099053
 ; Patent No. 6388063
 ; GENERAL INFORMATION:
 ; APPLICANT: Greg Plowman
 ; APPLICANT: Susan Onrust
 ; APPLICANT: David Markby
 ; APPLICANT: Sara Courtneidge
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
 ; TITLE OF INVENTION: SAD RELATED DISORDERS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/099,053
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/049,914
 ; FILING DATE: June 18, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 235/121
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; OTHER INFORMATION: "Xaa" in position 3 stands for
 ; OTHER INFORMATION: either Glu or Asp.
 ; US-09-099-053-3

Query Match 69.6%; Score 16; DB 4; Length 5;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FXXLW 5
 |||||
 Db 1 FGXWV 5

RESULT 6

US-07-893-930-37
 ; Sequence 37, Application US/07893930
 ; Patent No. 5317014
 ; GENERAL INFORMATION:

```

; APPLICANT: Fauchere, Jean-luc
; APPLICANT: Kucharczyk, Nathalie
; APPLICANT: Morris, Angela D.
; APPLICANT: Paladino, Joseph
; APPLICANT: Bonnet, Jacqueline
; APPLICANT: Thureau, Christophe
; TITLE OF INVENTION: NEW PEPTIDES AND PSEUDO-
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gordon W. Hueschen
; STREET: 715 The "H" Bldg., 310 East Michigan
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/893,930
; FILING DATE: 19920603
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91.06721
; FILING DATE: 04-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hueschen, Gordon W.
; REGISTRATION NUMBER: 16,157
; REFERENCE/DOCKET NUMBER: ADIR128/dlk
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-382-0030
; TELEFAX: 616-382-2030
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Benzhydryl
; OTHER INFORMATION: carbonyl"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: /note= "Abo"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /note= "NH2"
; US-07-893-930-37

```

```

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 LW 5
Db 3 LW 4

```

```

RESULT 7
US-08-073-028-44
; Sequence 44, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:

```

```

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELETYPE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-44

```

```

Query Match 65.2%; Score 15; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 LW 5
Db 1 LW 2

```

```

RESULT 8
US-08-133-011-148
; Sequence 148, Application US/08133011
; Patent No. 5658727
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray
; APPLICANT: Barbas, Carlos
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
; TITLE OF INVENTION: PHAGEMIDS
; NUMBER OF SEQUENCES: 161
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,011

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; FILING DATE: 08-JUN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/683,602
 ; FILING DATE: 10-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/826,623
 ; FILING DATE: 27-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US 92/03091
 ; FILING DATE: 10-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: SCRF 238.2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 148:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-133-011-148

Query Match 65.2%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

DB 4 LW 5

RESULT 9

; US-08-584-579-11
 ; Sequence 11, Application US/08584579
 ; Patent No. 5674979
 ; GENERAL INFORMATION:
 ; APPLICANT: Schramm, Wolfgang
 ; APPLICANT: Schramm, Hans J.
 ; TITLE OF INVENTION: Agent For Inhibiting Symmetrical
 ; TITLE OF INVENTION: Proteins, In Particular Enzymes
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/584,579
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/332,447
 ; FILING DATE: 31-OCT-1994
 ; APPLICATION NUMBER: US 08/112,215
 ; FILING DATE: 26-AUG-1993
 ; APPLICATION NUMBER: US 07/976,003
 ; FILING DATE: 13-NOV-1992
 ; APPLICATION NUMBER: US 07/585,141
 ; FILING DATE: 07-DEC-1990
 ; APPLICATION NUMBER: WO PCT/EP90/00219
 ; FILING DATE: 09-FEB-1990

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 39 04 040.2
 ; FILING DATE: 10-FEB-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Innen, Jeffrey L.
 ; REGISTRATION NUMBER: 28957
 ; REFERENCE/DOCKET NUMBER: 18644-96040
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: YES
 ; US-08-584-579-11

Query Match 65.2%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

DB 1 LW 2

RESULT 10

; US-08-704-170-103
 ; Sequence 103, Application US/08704170
 ; Patent No. 5707626
 ; GENERAL INFORMATION:
 ; APPLICANT: Douvas, Angeline
 ; APPLICANT: Takehana, Yoshi
 ; APPLICANT: Ehresmann, Glenn
 ; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
 ; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
 ; NUMBER OF SEQUENCES: 121
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 No. 5707626th Figueroa Street, Suite 500
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/704,170
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/029,850
 ; FILING DATE: 11-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Spitals, John P.
 ; REGISTRATION NUMBER: 29,215
 ; REFERENCE/DOCKET NUMBER: 1920-331
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 977-1001
 ; TELEFAX: (213) 977-1003
 ; INFORMATION FOR SEQ ID NO: 103:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-704-170-103

Query Match 65.2%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0;
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LW 5
 ||
 Db 4 LW 5

RESULT 11
 US-08-747-137-44
 ; Sequence 44, Application US/08747137
 ; Patent No. 5945033
 ; GENERAL INFORMATION:
 ; APPLICANT: YEN, Richard C.K.
 ; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
 ; NUMBER OF SEQUENCES: 184
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/747,137
 ; FILING DATE: 12-NOV-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,546
 ; FILING DATE: 14-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/069,831
 ; FILING DATE: 01-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/959,560
 ; FILING DATE: 13-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/641,720
 ; FILING DATE: 15-JAN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 016197-000840US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; US-08-747-137-44

Query Match 65.2%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0;
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LW 5
 ||
 Db 2 LW 3

RESULT 12
 US-08-530-326-14
 ; Sequence 14, Application US/08530326
 ; Patent No. 5961954

; GENERAL INFORMATION:
 ; APPLICANT: HILGER, CHRISTOPH-STEPH
 ; APPLICANT: DINKELBORG, LUDGER
 ; APPLICANT: KRAMP, WOLFGANG
 ; APPLICANT: SCHIER, HANS-MARTIN
 ; TITLE OF INVENTION: CHELATORS OF TYPE XN1S101 FOR RADIOACTIVE ISOTOPES, 7H
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLIESLER, DUBB, MEYER & LOVEJOY
 ; STREET: Four Embarcadero Center, Suite 400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/530,326
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DE94/00372
 ; FILING DATE: 29-MAR-1994
 ; APPLICATION NUMBER: P 43 10 999.3
 ; FILING DATE: 31-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dubb, Hubert E
 ; REGISTRATION NUMBER: 25,329
 ; REFERENCE/DOCKET NUMBER: WBLT 2006 (WO) PA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-362-3800
 ; TELEFAX: 415-362-2928
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-530-326-14

Query Match 65.2%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05; Indels 0;
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LW 5
 ||
 Db 4 LW 5

RESULT 13
 US-08-854-187A-2
 ; Sequence 2, Application US/08854187A
 ; Patent No. 5962642
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsugita, Akira
 ; TITLE OF INVENTION: Method for Sequencing of
 ; TITLE OF INVENTION: Protein or Peptide
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Adams & Wilks
 ; STREET: 50 Broadway, 31st Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America


```
Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      1 LW 2

RESULT 16
US-08-981-122-15
; Sequence 15, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide
; OTHER INFORMATION: synthesizing system (RAMPS)
US-08-981-122-15

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      1 LW 2

RESULT 17
US-08-981-122-38
; Sequence 38, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Examples 11 and 12 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
```

```
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-38

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 18
US-08-981-122-43
; Sequence 43, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 5
; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-43

Query Match      65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
      ||
Db      4 LW 5

RESULT 19
US-08-981-122-51
; Sequence 51, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

NAME/KEY: AMIDATION

LOCATION: 5
OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-fod
Patent No. 6127339
OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
US-08-981-122-51

Query Match 65.2%; Score 15; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 4 LW 5

RESULT 20

US-08-554-616-44
Sequence 44, Application US/08554616
Patent No. 6133418
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-44

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 1 LW 2

RESULT 21

US-08-530-342A-14
Sequence 14, Application US/08530342A
Patent No. 6143275
GENERAL INFORMATION:
APPLICANT: HILGER, CHRISTOPH-STEPH
APPLICANT: DINKELBORG, LUDGER
APPLICANT: KRAMP, WOLFGANG
APPLICANT: SCHIER, HANS-MARTIN
TITLE OF INVENTION: TYPE S3N2 CHELATORS FOR RADIO
TITLE OF INVENTION: ACTIVE ISOTOPES, THEIR METAL COMPLEXES AND
TITLE OF INVENTION: THEIR DIAGNOSTIC AND THERAPEUTICAL USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK &
ADDRESSEE: MORTIMER
STREET: 500 West Madison Street, Suite 3800
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60661-2511
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: COMPAQ Prolinea 4/25s
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect for Windows 6.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,342A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE94/00370
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: P 43 11 022.3
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mortimer, John S.
REGISTRATION NUMBER: 30,407
REFERENCE/DOCKET NUMBER: 1214.00008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/876-1800
TELEFAX: 312/876-2020
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-530-342A-14

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 4 LW 5

RESULT 22

US-09-208-277-9
Sequence 9, Application US/09208277
Patent No. 6166177
GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT AND DIAGNOSIS

```
; TITLE OF INVENTION: OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469
; CURRENT APPLICATION NUMBER: US/09/208,277
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-208-277-9

Query Match          65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 3 LW 4

RESULT 23
US-08-907-739-148
; Sequence 148, Application US/08907739
; Patent No. 6235469
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray
; APPLICANT: Barbas, Carlos
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
; TITLE OF INVENTION: PHAGEMIDS
; NUMBER OF SEQUENCES: 161
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,739
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,011
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US 92/03091
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRF 238.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-907-739-148
```

```
Query Match          65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 4 LW 5

RESULT 24
US-09-082-279B-791
; Sequence 791, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-791
```

```
Query Match          65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
DB 1 LW 2

RESULT 25
US-09-315-304B-791
; Sequence 791, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 791
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-791
```

```
Query Match          65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 1 LW 2

RESULT 26

US-09-556-877-9
; Sequence 9, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-556-877-9

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 27

US-09-288-594A-9
; Sequence 9, Application US/09288594A
; Patent No. 6447779
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TREATMENT
; FILE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C1
; CURRENT APPLICATION NUMBER: US/09/288,594A
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-288-594A-9

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 28

US-09-620-412C-9
; Sequence 9, Application US/09620412C

Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-620-412C-9

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 3 LW 4

RESULT 29

US-08-469-260A-228
; Sequence 228, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; FILE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 228:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-228

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LW 5
||
Db 3 LW 4

RESULT 30

US-09-729-597-148
; Sequence 148, Application US/09729597
; Patent No. 6468738
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray
; Barbas, Carlos
; Lerner, Richard A.
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
; PHAGEMIDS
; NUMBER OF SEQUENCES: 161
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,597
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,011
; FILING DATE: 1994-09-29
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; APPLICATION NUMBER: PCT/US 92/03091
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRF 238.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-09-729-597-148

Query Match 65.2%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LW 5
||
Db 4 LW 5

RESULT 31
PCT-US94-01321-47
; Sequence 47, Application PC/TUS9401321
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 72
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01321
; FILING DATE: 04-FEB-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156551
; FILING DATE: 22-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014431
; FILING DATE: 05-FEB-1993
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-01321-47

Query Match 65.2%; Score 15; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0;
Qy 4 LW 5
||
Db 3 LW 4

RESULT 32

PCT-US94-02631-103
; Sequence 103, Application PC/TUS9402631
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
; IMMUNOINFECTIVE CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02631
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215

; REFERENCE/DOCKET NUMBER: 1920-331
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 977-1001
 ; TELEFAX: (213) 977-1003
 ; INFORMATION FOR SEQ ID NO: 103:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 PCT-US94-02631-103

Query Match 65.2%; Score 15; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 4 LW 5

RESULT 33

5171838-3
 ; Patent No. 5171838
 ; APPLICANT: CHIBA, YUKINOBU
 ; TITLE OF INVENTION: LEUJA BINDING PEPTIDES
 ; NUMBER OF SEQUENCES: 24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/526,921
 ; FILING DATE: 22-MAY-1990
 ; SEQ ID NO:3:
 ; LENGTH: 5
 5171838-3

Query Match 65.2%; Score 15; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
 Db 3 LW 4

RESULT 34

US-07-789-184-83
 ; Sequence 83, Application US/07789184
 ; Patent No. 5688768
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/789,184
 ; FILING DATE: 19911107
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.20

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 34-0154
 ; INFORMATION FOR SEQ ID NO: 83:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-07-789-184-83

Query Match 60.9%; Score 14; DB 1; Length 5;
 Best Local Similarity 40.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 Db 1 FEPFW 5

RESULT 35

US-08-475-263-83
 ; Sequence 83, Application US/08475263
 ; Patent No. 5759994
 ; GENERAL INFORMATION:
 ; APPLICANT: COUGHLIN, SHAUN R.
 ; APPLICANT: SCARBOROUGH, ROBERT M.
 ; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 ; TITLE OF INVENTION: RELATED PHARMACEUTICALS
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 2000 Pennsylvania Ave., NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,263
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 22000-20502.03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500
 ; TELEFAX: (202) 887-0763
 ; TELEX: 90-4030
 ; INFORMATION FOR SEQ ID NO: 83:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-475-263-83

Query Match 60.9%; Score 14; DB 1; Length 5;
 Best Local Similarity 40.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 Db 1 FEPFW 5

RESULT 36

US-08-485-886-83	US-08-477-362-83	US-08-485-886-83	US-08-477-362-83
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,362	APPLICATION NUMBER: US/08/477,362	APPLICATION NUMBER: US/08/477,362	APPLICATION NUMBER: US/08/477,362
FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995
CLASSIFICATION: 435	CLASSIFICATION: 435	CLASSIFICATION: 435	CLASSIFICATION: 435
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184	APPLICATION NUMBER: US 07/789,184	APPLICATION NUMBER: US 07/789,184	APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991	FILING DATE: 07-NOV-1991	FILING DATE: 07-NOV-1991	FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.	NAME: MURASHIGE, KATE H.	NAME: MURASHIGE, KATE H.	NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959	REGISTRATION NUMBER: 29,959	REGISTRATION NUMBER: 29,959	REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20	REFERENCE/DOCKET NUMBER: 22000-20502.20	REFERENCE/DOCKET NUMBER: 22000-20502.20	REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600	TELEPHONE: (415) 813-5600	TELEPHONE: (415) 813-5600	TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792	TELEFAX: (415) 494-0792	TELEFAX: (415) 494-0792	TELEFAX: (415) 494-0792
TELEX: 34-0154	TELEX: 34-0154	TELEX: 34-0154	TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 83:	INFORMATION FOR SEQ ID NO: 83:	INFORMATION FOR SEQ ID NO: 83:	INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids	LENGTH: 5 amino acids	LENGTH: 5 amino acids	LENGTH: 5 amino acids
TYPE: amino acid	TYPE: amino acid	TYPE: amino acid	TYPE: amino acid
STRANDEDNESS: single	STRANDEDNESS: single	STRANDEDNESS: single	STRANDEDNESS: single
TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear	TOPOLOGY: linear
US-08-477-362-83	US-08-477-362-83	US-08-477-362-83	US-08-477-362-83
Query Match 60.9%; Score 14; DB 2; Length 5;	Query Match 60.9%; Score 14; DB 2; Length 5;	Query Match 60.9%; Score 14; DB 1; Length 5;	Query Match 60.9%; Score 14; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;	Best Local Similarity 40.0%; Pred. No. 2e+05;	Best Local Similarity 40.0%; Pred. No. 2e+05;	Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXLW 5	Qy 1 FXXLW 5	Qy 1 FXXLW 5	Qy 1 FXXLW 5
Db 1 PEPFW 5	Db 1 PEPFW 5	Db 1 PEPFW 5	Db 1 PEPFW 5
RESULT 38	RESULT 38	RESULT 37	RESULT 37
US-08-477-134-83	US-08-477-134-83	US-08-477-362-83	US-08-477-362-83
Sequence 83, Application US/08477134	Sequence 83, Application US/08477134	Sequence 83, Application US/08477362	Sequence 83, Application US/08477362
Patent No. 5856448	Patent No. 5856448	Patent No. 5849507	Patent No. 5849507
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.	APPLICANT: COUGHLIN, SHAUN R.	APPLICANT: COUGHLIN, SHAUN R.	APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.	APPLICANT: SCARBOROUGH, ROBERT M.	APPLICANT: SCARBOROUGH, ROBERT M.	APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND	TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND	TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND	TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS	TITLE OF INVENTION: RELATED PHARMACEUTICALS	TITLE OF INVENTION: RELATED PHARMACEUTICALS	TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223	NUMBER OF SEQUENCES: 223	NUMBER OF SEQUENCES: 223	NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER	ADDRESSEE: MORRISON & FOERSTER	ADDRESSEE: MORRISON & FOERSTER	ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road	STREET: 755 Page Mill Road	STREET: 755 Page Mill Road	STREET: 755 Page Mill Road
CITY: Palo Alto	CITY: Palo Alto	CITY: Palo Alto	CITY: Palo Alto
STATE: California	STATE: California	STATE: California	STATE: California
COUNTRY: USA	COUNTRY: USA	COUNTRY: USA	COUNTRY: USA
ZIP: 94304-1018	ZIP: 94304-1018	ZIP: 94304-1018	ZIP: 94304-1018
COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25	SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,886	APPLICATION NUMBER: US/08/485,886	APPLICATION NUMBER: US/08/485,886	APPLICATION NUMBER: US/08/485,886
FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995
CLASSIFICATION: 435	CLASSIFICATION: 435		

;
;
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-477-134-83

Query Match 60.9%; Score 14; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FEPFW 5

RESULT 39

US-08-473-489A-83
; Sequence 83, Application US/08473489A
; Patent No. 6024936

GENERAL INFORMATION:

;
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/473.489A

FILING DATE:

;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184

FILING DATE:

;
; FILING DATE: 1991-11-07
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20

TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154

INFORMATION FOR SEQ ID NO: 83:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-473-489A-83

Query Match 60.9%; Score 14; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FEPFW 5

RESULT 40

US-08-485-695-83
; Sequence 83, Application US/08485695
; Patent No. 6124101

;
;
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/485,695
; FILING DATE: 07-JUN-1995

CLASSIFICATION:

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991

ATTORNEY/AGENT INFORMATION:

;
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154

INFORMATION FOR SEQ ID NO: 83:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-695-83

Query Match 60.9%; Score 14; DB 3; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
|
Db 1 FEPFW 5

RESULT 41

US-08-018-760-83

;
; Sequence 83, Application US/08018760
; Patent No. 6197541

GENERAL INFORMATION:

;
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/08/018,760
; FILING DATE: 17-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-018-760-83

Query Match 60.9%; Score 14; DB 4; Length 5;
Best Local Similarity 40.0%; Pred. No. 2e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 1 FEPFW 5

RESULT 42
US-07-858-842-3
; Sequence 3, Application US/07858842
; Patent No. 5314807
; GENERAL INFORMATION:
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yokoyama, Keiichi
; APPLICANT: Hasegawa, Masayasu
; APPLICANT: Yasumoto, Ryouichi
; APPLICANT: Fujita, Hiroyuki
; TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARMSTRONG & KUBOVCIK
; STREET: 1725 K Street N.W., Suite 1000
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: United States of America
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/858,842
; FILING DATE: 19920327
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 142283
; FILING DATE: 29-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 298060
; FILING DATE: 17-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34, 409
; REFERENCE/DOCKET NUMBER: 920247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
```

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-07-858-842-3

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 1 IW 2

RESULT 43
US-07-960-636B-2
; Sequence 2, Application US/07960636B
; Patent No. 5369015
; GENERAL INFORMATION:
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yokoyama, Keiichi
; APPLICANT: Hasegawa, Masayasu
; APPLICANT: Yasumoto, Ryouichi
; APPLICANT: Fujita, Hiroyuki
; TITLE OF INVENTION: Method for Producing an Angiotensin
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
; ADDRESSEE: Naughton
; STREET: 1725 K Street, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/960,636B
; FILING DATE: 14-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 298061/1991
; FILING DATE: 17-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tockman, Albert
; REGISTRATION NUMBER: 19722
; REFERENCE/DOCKET NUMBER: P1161-2679-A920798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mammalian meat, fish, crustaceans
; US-07-960-636B-2

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
```

```

Db      1 IW 2
;
; TITLE OF INVENTION: NEW HEXAPEPTIDIC
; TITLE OF INVENTION: DERIVATIVES, PREPARATION, METHOD AND
; TITLE OF INVENTION: APPLICATION AS MEDICATIONS OF SAID NEW
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT # 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,020
; FILING DATE: 03-DEC-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146,1195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-661-8000
; TELEFAX: 212-661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: AMINO ACID
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; US-08-133-020-4

Query Match          56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0

Qy      4 LW 5
;
; Db      4 IW 5
;
; RESULT 46
; US-07-802-667-19
; Sequence 19, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667

Db      1 IW 2
;
; TITLE OF INVENTION: Val-resin
; TITLE OF INVENTION: The carboxy terminal amino acid, Val, is
; attached to a resin"
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSES: No. 5464935ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,680
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 891,986
; FILING DATE: 05-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Elderkin, Dianne B.
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; TELEX: 710-670-1334
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Val-resin
; OTHER INFORMATION: /note="The carboxy terminal amino acid, Val, is
; attached to a resin"
; US-08-384-680-8

Query Match          56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4 LW 5
;
; Db      1 IW 2
;
; RESULT 45
; US-08-133-020-4
; Sequence 4, Application US/08133020
; Patent No. 5476840
; GENERAL INFORMATION:
; APPLICANT: PIERRE BROTO, ET AL.
```

```
; FILING DATE: 19911205
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BELLAMY, ELIZABETH A.
; REGISTRATION NUMBER: 27,854
; REFERENCE/DOCKET NUMBER: BERLEX 51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-305-5472
; TELEFAX: 201-305-4405
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-TERMINAL N-ACETYL"
;
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /note= "C-TERMINAL AMIDE ESTER"
;
; US-07-802-667-20
;
; Query Match 56.5%; Score 13; DB 1; Length 5;
; Best Local Similarity 50.0%; Pred. No. 2e+05;
; Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 LW 5
; :|
; Db 3 IW 4
;
; RESULT 47
; US-07-802-667-20
; Sequence 20, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667
; FILING DATE: 19911205
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BELLAMY, ELIZABETH A.
; REGISTRATION NUMBER: 27,854
; REFERENCE/DOCKET NUMBER: BERLEX 51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-305-5472
; TELEFAX: 201-305-4405
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-TERMINAL N-ACETYL"
;
; FEATURE:
; NAME/KEY: Modified-site
;
; US-07-802-667-19
;
; Query Match 56.5%; Score 13; DB 1; Length 5;
; Best Local Similarity 50.0%; Pred. No. 2e+05;
; Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 LW 5
; :|
; Db 3 IW 4
;
; RESULT 48
; US-07-802-667-21
; Sequence 21, Application US/07802667
; Patent No. 5504070
; GENERAL INFORMATION:
; APPLICANT: BIHOVSKY, RON H.
; APPLICANT: ERHARDT, PAUL W.
; APPLICANT: LAMPE, JOHN W.
; APPLICANT: MOHAN, RAJU
; APPLICANT: SHAW, KENNETH J.
; TITLE OF INVENTION: INHIBITORS OF THE CONVERSION OF BIG
; TITLE OF INVENTION: ENDOTHELIN TO ENDOTHELIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERLEX LABORATORIES, INC.
; STREET: 300 FAIRFIELD ROAD
; CITY: WAYNE
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07470-5472
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/802,667
; FILING DATE: 19911205
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BELLAMY, ELIZABETH A.
; REGISTRATION NUMBER: 27,854
; REFERENCE/DOCKET NUMBER: BERLEX 51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-305-5472
; TELEFAX: 201-305-4405
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-TERMINAL N-ACETYL"
;
; FEATURE:
; NAME/KEY: Modified-site
```

; LOCATION: 5
; OTHER INFORMATION: /note= "C-TERMINAL AMIDE ESTER"
; US-07-802-667-21

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 3 IW 4

RESULT 49

US-08-057-167-12
; Sequence 12, Application US/08057167
; Patent No. 5541095
; GENERAL INFORMATION:
; APPLICANT: Hirschberg, Carlos B.
; APPLICANT: Orellana, Ariel
; APPLICANT: Hashimoto, Yasuhiro
; APPLICANT: Swiedler, Stuart J.
; APPLICANT: Wei, Zheng
; APPLICANT: Ishihara, Masayuki
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN SPECIFIC
; TITLE OF INVENTION: SULFOTRANSFERASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/057,167
FILING DATE: 19930430

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,432
FILING DATE: 16 June 1992
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04020/015002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: AMINO ACID
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-057-167-12

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 2 IW 3

RESULT 50

US-08-269-257-9

; Sequence 9, Application US/08269257
; Patent No. 5550110
; GENERAL INFORMATION:
; APPLICANT: Cody, Wayne L.
; APPLICANT: Doherty, Annette M.
; APPLICANT: Topliss, John G.
; TITLE OF INVENTION: Endothelin Antagonists II
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ver. #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,257
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,515
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Tinney, Francis J.
REGISTRATION NUMBER: 33069
REFERENCE/DOCKET NUMBER: PD-4334-P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-7295
TELEFAX: 313 996-1553

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-257-9

Query Match 56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 4 IW 5

RESULT 51

US-08-373-911-5
; Sequence 5, Application US/08373911
; Patent No. 5663296
; GENERAL INFORMATION:
; APPLICANT: Doherty, Annette M.
; APPLICANT: Kornberg, Brian E.
; APPLICANT: Nikam, Sham S.
; TITLE OF INVENTION: Hydroxamate Inhibitors of
; TITLE OF INVENTION: Endothelin Converting Enzyme
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,911
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33069
; REFERENCE/DOCKET NUMBER: PD-4435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-373-911-5

```

```

Query Match      56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 LW 5
   :|
Db 4 IW 5

```

```

RESULT 52
US-08-373-911-6
; Sequence 6, Application US/08373911
; Patent No. 5663296
; GENERAL INFORMATION:
; APPLICANT: Doherty, Annette M.
; APPLICANT: Kornberg, Brian E.
; APPLICANT: Nikam, Sham S.
; TITLE OF INVENTION: Hydroxamate Inhibitors of
; TITLE OF INVENTION: Endothelin Converting Enzyme
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,911
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33069
; REFERENCE/DOCKET NUMBER: PD-4435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-373-911-6

```

```

Query Match      56.5%; Score 13; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 4 LW 5
   :|
Db 4 IW 5

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```

RESULT 53
US-08-483-506A-1
; Sequence 1, Application US/08483506A
; Patent No. 5925529
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, ET AL.
; TITLE OF INVENTION: METHOD FOR DISCOVERY OF PEPTIDE AGONISTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP
; STREET: FIVE PALO ALTO SQUARE
; STREET: 3000 EL CAMINO REAL
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,506A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY, RICHARD L. PhD
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-239/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5000
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-506A-1

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Query Match      56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 LW 5
   :|
Db 2 MW 3

```

```

RESULT 54
US-08-483-506A-2
; Sequence 2, Application US/08483506A
; Patent No. 5925529
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, ET AL.
; TITLE OF INVENTION: METHOD FOR DISCOVERY OF PEPTIDE AGONISTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD LLP

```

```
; STREET: FIVE PALO ALTO SQUARE
; STREET: 3000 EL CAMINO REAL
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483.506A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEELEY, RICHARD L. PhD
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-239/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5000
; TELEFAX: (415) 857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Should be Formyl-Met"
;
US-08-483-506A-2

Query Match 56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 2 MW 3

RESULT 55
US-08-437-607A-38
; Sequence 38, Application US/08437607A
; Patent No. 5955579
; GENERAL INFORMATION:
; APPLICANT: Leonard, James N. Montminy, Marc R.
; TITLE OF INVENTION: ISLET-SPECIFIC HOMOPROTEIN AND TRANSCRIPTIONAL
; TITLE OF INVENTION: REGULATOR OF INSULIN GENE EXPRESSION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437.607A
; FILING DATE: MAY 9, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1110-1-001
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: amino acids 47-51 of the homeobox homeodomain
; ORIGINAL SOURCE:
; ORGANISM: Rat
;
US-08-437-607A-38

Query Match 56.5%; Score 13; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 1 IW 2

RESULT 56
US-08-981-122-2
; Sequence 2, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/JP96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
; Patent No. 6127339
; OTHER INFORMATION: F-moc amino acids by solid phase method using a multipetide
; OTHER INFORMATION: synthesizing system (RAMPS)
;
US-08-981-122-2

Query Match 56.5%; Score 13; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
Db 3 IW 4

RESULT 57
US-08-981-122-19
; Sequence 19, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Aritomi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
```

; PRIOR APPLICATION NUMBER: PCT/JP96/01734
 ; PRIOR FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence of a peptide synthesized in Example 2 from L-form
 ; Patent No. 6127339
 ; OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide
 ; OTHER INFORMATION: synthesizing system (RAMPS)
 US-08-981-122-19

Query Match 56.5%; Score 13; DB 3; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 :
 Db 3 MW 4

RESULT 58
 US-08-981-122-37
 ; Sequence 37, Application US/08981122B
 ; Patent No. 6127339
 ; GENERAL INFORMATION:
 ; APPLICANT: Hatanaka, Yoshihiro
 ; APPLICANT: Aritomi, Masaharu
 ; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/08/981,122B
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: JP 7-176904
 ; PRIOR FILING DATE: 1995-06-21
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01734
 ; PRIOR FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 37
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: AMIDATION
 ; LOCATION: 5
 ; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
 ; Patent No. 6127339
 ; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
 ; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
 US-08-981-122-37

Query Match 56.5%; Score 13; DB 3; Length 5;
 Best Local Similarity 40.0%; Pred. No. 2e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
 :
 Db 1 FFFRW 5

RESULT 59
 US-08-981-122-53
 ; Sequence 53, Application US/08981122B
 ; Patent No. 6127339
 ; GENERAL INFORMATION:
 ; APPLICANT: Hatanaka, Yoshihiro
 ; APPLICANT: Aritomi, Masaharu
 ; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/08/981,122B

; CURRENT FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: JP 7-176904
 ; PRIOR FILING DATE: 1995-06-21
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01734
 ; PRIOR FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 53
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: AMIDATION
 ; LOCATION: 5
 ; OTHER INFORMATION: Sequence of peptides synthesized in Examples 11 and 12 from L-form
 ; Patent No. 6127339
 ; OTHER INFORMATION: F-moc amino acids by solid phase method using an automatic peptide
 ; OTHER INFORMATION: synthesizer (9050 plus peptide synthesizer)
 US-08-981-122-53

Query Match 56.5%; Score 13; DB 3; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 :
 Db 4 IW 5

RESULT 60
 US-08-981-122-72
 ; Sequence 72, Application US/08981122B
 ; Patent No. 6127339
 ; GENERAL INFORMATION:
 ; APPLICANT: Hatanaka, Yoshihiro
 ; APPLICANT: Aritomi, Masaharu
 ; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/08/981,122B
 ; CURRENT FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: JP 7-176904
 ; PRIOR FILING DATE: 1995-06-21
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01734
 ; PRIOR FILING DATE: 1996-06-21
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 72
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 2 from
 ; Patent No. 6127339
 ; OTHER INFORMATION: L-form F-moc amino acids by solid phase method using a
 ; OTHER INFORMATION: multi-peptide synthesizing system (RAMPS)
 US-08-981-122-72

Query Match 56.5%; Score 13; DB 3; Length 5;
 Best Local Similarity 20.0%; Pred. No. 2e+05;
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0,

QY 1 FXXLW 5
 :
 Db 1 YIQWV 5

RESULT 61
 US-08-871-600A-4
 ; Sequence 4, Application US/08871600A
 ; Patent No. 6222021
 ; GENERAL INFORMATION:
 ; APPLICANT: Wainwright, No. 6222021man R.
 ; APPLICANT: No. 6222021itsky, Thomas J.

;; TITLE OF INVENTION: Endotoxin Binding and Neutralizing
;; TITLE OF INVENTION: Protein and Uses Thereof
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: District of Columbia
;; COUNTRY: United States of America
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/871,600A
;; FILING DATE: 09-JUN-1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/704,872
;; FILING DATE: 30-AUG-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/264,244
;; FILING DATE: 22-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/883,457
;; FILING DATE: 15-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,501
;; FILING DATE: 16-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/480,957
;; FILING DATE: 16-FEB-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/210,575
;; FILING DATE: 23-JUN-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Esmond, Robert W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 1413.001000A/RWE
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; TELEX: 248636 SSK
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-871-600A-4
Query Match 56.5%; Score 13; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 3 IW 4
RESULT 62
US-09-216-295-26
; Sequence 26, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295

;; CURRENT FILING DATE: 1998-12-18
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 26
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE: Peptide
;; OTHER INFORMATION: Peptide
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(5)
;; OTHER INFORMATION: Xaa = Leu, Phe, or Ile
US-09-216-295-26
Query Match 56.5%; Score 13; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 4 IW 5
RESULT 63
US-09-638-202A-51
; Sequence 51, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koeda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-638-202A-51
Query Match 56.5%; Score 13; DB 4; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 2 MW 3

RESULT 64

PCT-US93-05412-12
; Sequence 12, Application PC/TUS9305412
; GENERAL INFORMATION:
; APPLICANT: Hirschberg, Carlos B.
; APPLICANT: Orellana, Ariel
; APPLICANT: Hashimoto, Yasuhiro
; APPLICANT: Swiedler, Stuart J.
; APPLICANT: Wei, Zheng
; APPLICANT: Ishihara, Masayuki
; TITLE OF INVENTION: GLYCOSAMINOGLYCAN SPECIFIC
; TITLE OF INVENTION: SULFOTRANSFERASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05412
; FILING DATE: 19930607
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/899,432
; FILING DATE: 16 June 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, PAUL T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04020/015002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
PCT-US93-05412-12

Query Match 56.5%; Score 13; DB 5; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 2 IW 3

RESULT 65

PCT-US95-04171-9
; Sequence 9, Application PC/TUS9504171
; GENERAL INFORMATION:
; APPLICANT: Cody, Wayne L.
; APPLICANT: Doherty, Annette M.
; APPLICANT: Topliss, John G.
; TITLE OF INVENTION: Endothelin Antagonists II
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Ver. #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04171
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,515
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Timney, Francis J.
; REGISTRATION NUMBER: 33069
; REFERENCE/DOCKET NUMBER: PD-4334-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-04171-9

Query Match 56.5%; Score 13; DB 5; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 4 IW 5

RESULT 66
5217869-16
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:16:
; LENGTH: 5
5217869-16

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
:|
Db 2 MW 3

RESULT 67

5217869-22
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:22:
; LENGTH: 5
5217869-22

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
;:
Db 1 MW 2

RESULT 68
5217869-24
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:24:
; LENGTH: 5
5217869-24

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
;:
Db 3 MW 4

RESULT 69
5217869-34
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:34:
; LENGTH: 5
5217869-34

Query Match 56.5%; Score 13; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
;:
Db 1 MW 2

RESULT 70
US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalampos
; APPLICANT: Franz, Gerald H
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,237
; FILING DATE: 19920914
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: David E. Brook
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BT192-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; MOLECULE TYPE: peptide
US-07-946-237-4

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
;:
Db 2 VW 3

RESULT 71
US-08-290-448A-3
; Sequence 3, Application US/08290448A
; Patent No. 5676954
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mei-Chang
; TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,448A
; FILING DATE: August 15, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: May 29, 1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: March 17, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-3

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 1 VW 2

RESULT 72
US-08-290-448A-39
Sequence 39, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-39

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5

Db 1 VW 2

RESULT 73
US-08-064-111C-22
Sequence 22, Application US/08064111C
Patent No. 5688760
GENERAL INFORMATION:
APPLICANT: Kemp, Bruce E.
APPLICANT: Nicholson, Geoffrey C.
APPLICANT: Martin, Thomas J.
APPLICANT: Fenton, Anna J.
APPLICANT: Hammonds, R. Glenn
TITLE OF INVENTION: COMPOUNDS AND COMPOSITIONS WHICH INHIBIT
TITLE OF INVENTION: BONE RESORPTION
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
ADDRESSEE: Attn: W.H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,111C
FILING DATE: 12-AUG-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00580
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK9567
FILING DATE: 19-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK3879
FILING DATE: 13-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58456/WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRADEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-064-111C-22

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 YRSAM 5

RESULT 74
US-08-290-448A-3
Sequence 3, Application US/08290448A
Patent No. 5698204

GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-3

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 1 VW 2

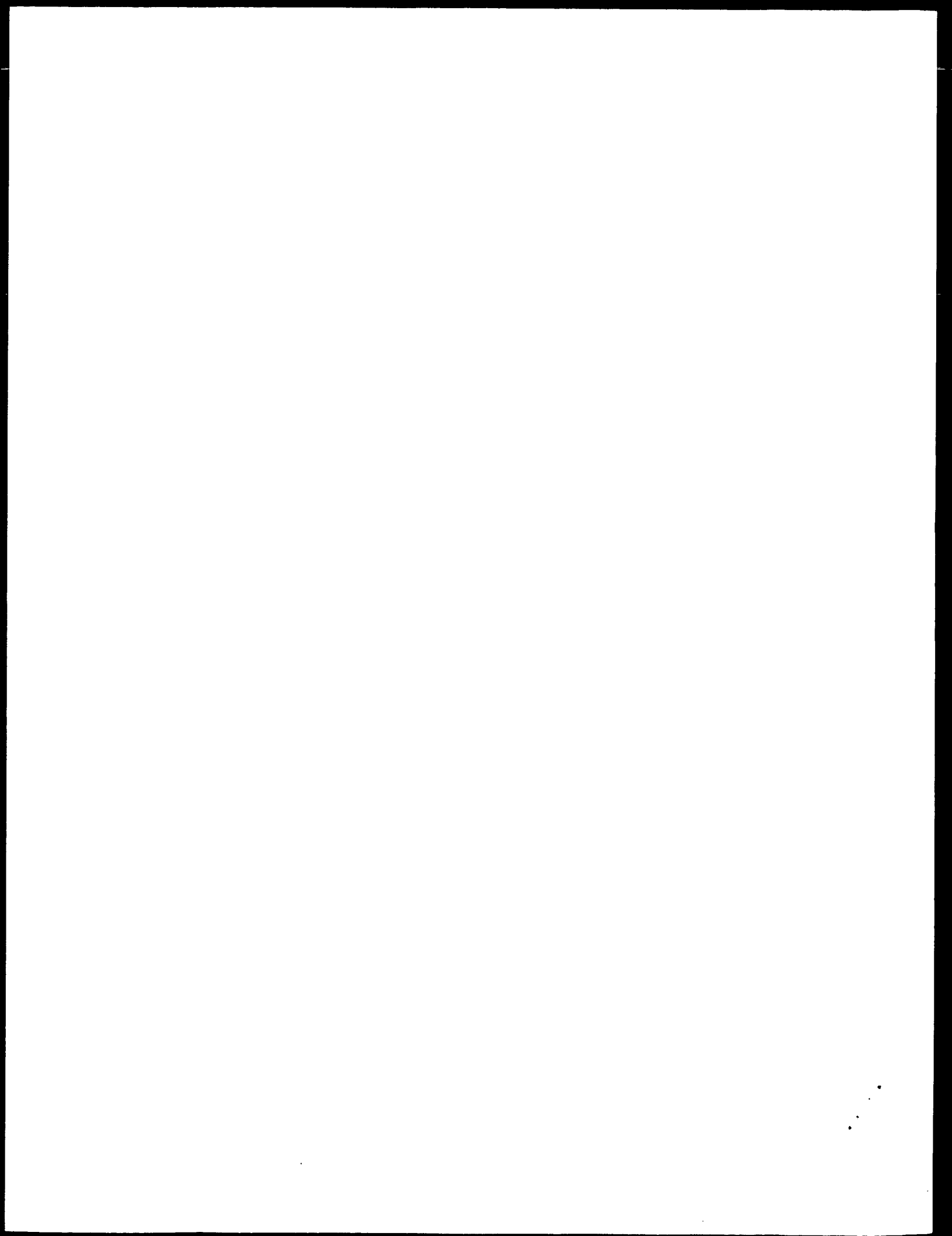
RESULT 75
US-08-290-448A-39
Sequence 39, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-290-448A-39

Query Match 52.2%; Score 12; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
:|
Db 1 VW 2

Search completed: February 12, 2003, 10:53:11
Job time : 15 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:22 ; Search time 5.41667 Seconds
(without alignments)
88.739 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 4984

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	87.0	15	2	PH1613
2	17	73.9	16	2	C37290
3	17	73.9	25	2	S68897
4	16	69.6	24	2	S38281
5	15	65.2	6	2	B34835
6	15	65.2	6	2	P70519
7	15	65.2	7	2	PH1602
8	15	65.2	8	2	A39308
9	15	65.2	9	2	A42444
10	15	65.2	9	2	S07241
11	15	65.2	10	2	B49033
12	15	65.2	10	2	F49033
13	15	65.2	11	1	LFTWE
14	15	65.2	11	2	C33652
15	15	65.2	12	2	A39169
16	15	65.2	12	2	I64829
17	15	65.2	12	2	A36093
18	15	65.2	12	2	I58273
19	15	65.2	13	2	PH1620
20	15	65.2	13	2	G37266
21	15	65.2	13	2	D37267
22	15	65.2	13	2	I51905
23	15	65.2	13	2	S54344
24	15	65.2	14	2	A35105
25	15	65.2	14	2	PH1625
26	15	65.2	14	2	PH1626
27	15	65.2	14	2	PH1627
28	15	65.2	14	2	PH1594
29	15	65.2	14	2	PH0801

Tcr delta chain V-
T cell receptor al
7 alpha-hydroxy-4-
Ig H chain V-D-J r
Ig H chain V-D-J r
Ig H chain V-D-J r
Tcr delta chain V-
hydrogenase (SC 1.
Ig H chain V-D-J r
Ig H chain V-D-J r
Tcr delta chain V-
transforming prote
caldesmon - rabbit
Ig H chain V-D-J r
T-cell receptor de
shikimate 5-dehydr
choline O-acetyl r

ALIGNMENTS

RESULT 1

PH1613

Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1613

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1613

A;Molecule type: DNA

A;Residues: 1-15 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 87.0%; Score 20; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5

Db 10 FTMLW 14

RESULT 2

C37290

homeotic protein Gsh-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 17-Oct-1997

C;Accession: C37290; C38809

R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter

Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991

A;Title: Identification of 10 murine homeobox genes.

A;Reference number: A37290; MUID:92073356; PMID:1683707

A;Accession: C37290

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-16 <SIN>

C;Superfamily: unassigned homeobox proteins; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;1-14/Domain: homeobox homology (fragment) <HOX>

Query Match 73.9%; Score 17; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 1e+03;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5

Db 12 FKXW 16

RESULT 3

S68897
 phospholipase A2 (EC 3.1.1.4), cytosolic - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999
 C;Accession: S68897
 R;Gordon, R.D.; Leighton, I.A.; Campbell, D.G.; Cohen, P.; Creaney, A.; Wilton, D.C.; Ma
 Eur. J. Biochem. 236, 690-697, 1996
 A;Title: Cloning and expression of cytosolic phospholipase A(2) (cPLA(2)) and a natural
 results in an increase in specific activity.
 A;Reference number: S68897; MUID:96300233; PMID:8706669
 A;Accession: S68897
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-25 <GOR>
 C;Keywords: carboxylic ester hydrolase; cytosol

Query Match 73.9%; Score 17; DB 2; Length 25;
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

: ||

Db 13 YMSLW 17

RESULT 4

S38281
 GTP-binding protein - clawed frog (fragments)
 C;Species: Xenopus sp. (clawed frog)
 C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 28-May-1999
 C;Accession: S38281
 R;Moore, M.S.; Blobel, G.
 Nature 365, 661-663, 1993
 A;Title: The GTP-binding protein Ran/TC4 is required for protein import into the nucleus
 A;Reference number: S38281; MUID:94019818; PMID:8413630
 A;Accession: S38281
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <MO>
 C;Superfamily: ras transforming protein; translation elongation factor Tu homology
 C;Keywords: GTP binding

Query Match 69.6%; Score 16; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

: ||

Db 13 FFNVW 17

RESULT 5

B34835
 dnaA protein - Pseudomonas aeruginosa (fragment)
 C;Species: Pseudomonas aeruginosa
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C;Accession: B34835
 R;Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
 A;Reference number: B34835; MUID:90160310; PMID:2106132
 A;Accession: B34835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <YEE>
 A;Cross-references: GB:M30125; NID:G151419; PIDN:AAA25916.1; PID:G151421.
 C;Keywords: DNA binding

Query Match 65.2%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

: ||

Db 5 LW 6

RESULT 6

PT0519
 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0519
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0519
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-6 <FE>
 A;Experimental source: adult thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 65.2%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

: ||

Db 4 LW 5

RESULT 7

PH1602
 Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PH1602
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387
 A;Accession: PH1602
 A;Molecule type: DNA
 A;Residues: 1-7 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 65.2%; Score 15; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

: ||

Db 5 LW 6

RESULT 8

A39308
 glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklan
 C;Species: Clostridium sticklandii
 C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C;Accession: A39308
 R;Stadtman, T.C.; Davis, J.N.
 J. Biol. Chem. 266, 22147-22153, 1991
 A;Title: Glycine reductase protein C. Properties and characterization of its role in the
 A;Reference number: A39308; MUID:92042141; PMID:1939235
 A;Accession: A39308
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <STA>
 C;Function:
 A;Description: glycine reductase complex catalyzes the reductive deamination of glycine
 C;Keywords: ATP; oxidoreductase

Query Match 65.2%; Score 15; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 65.2%; Score 15; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
5 LW 6

Db

RESULT 9
A24244
adipokinetic hormone - bollworm
N:Alternate names: Hez-AKH
C:Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
C>Date: 31-Mar-1998 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
Biochem. Biophys. Res. Commun. 135, 622-628, 1986
A:Title: Isolation and primary structure of a peptide from the corpora cardiaca of Heliothis zea
A:Reference number: A24244; MUID:86186794; PMID:3964263
A:Accession: A24244
A:Molecule type: protein
A:Residues: 1-9 <JAF>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
||
4 FTSSW 8

Db

RESULT 10
S07241
litorin - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07241
R:Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer,
FEBS Lett. 182, 53-56, 1985
A:Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
A:Reference number: S07241; MUID:85127560; PMID:3838283
A:Accession: S07241
A:Molecule type: protein
A:Residues: 1-9 <BAR>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
2 LW 3

Db

RESULT 11
E49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
C:Accession: E49033; D49033
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991

A:Title: Functionally distinct subsets of human gamma/delta T cells.

A:Reference number: A49033; MUID:92083926; PMID:1684157

A:Accession: E49033

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-10 <MOR>

A:Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697

A>Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)

A:Accession: D49033

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-10 <MOR2>

A:Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697

A>Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)

C:Keywords: T-cell receptor

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

||

3 LW 4

Db

RESULT 12

F49033

T-cell receptor gamma chain V-D-J region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: F49033

R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.

Eur. J. Immunol. 21, 2999-3007, 1991

A:Title: Functionally distinct subsets of human gamma/delta T cells.

A:Reference number: A49033; MUID:92083926; PMID:1684157

A:Accession: F49033

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-10 <MOR>

A:Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701

A>Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)

C:Keywords: T-cell receptor

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5

||

3 LW 4

Db

RESULT 13

LFTWWE

probable trpEG leader peptide - Thermus aquaticus

C:Species: Thermus aquaticus

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C:Accession: S03315

R:Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988

A:Title: Molecular cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and

A:Reference number: S03315; MUID:89000781; PMID:2844259

A:Accession: S03315

A:Molecule type: DNA

A:Residues: 1-11 <SAT>

A:Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262

A>Note: the source is designated as Thermus thermophilus HB8

C:Genetics:

A:Gene: trpL

C:Superfamily: probable trpEG leader peptide

Query Match 65.2%; Score 15; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 7 LW 8

RESULT 14

C53652
rhlR protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998
C:Accession: C53652
R:Ochsner, U.A.; Fiechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A:Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas
A:Reference number: A53652; MUID:94327521; PMID:8051059
A:Accession: C53652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <OCH>
A:Cross-references: GB:L28170
C:Superfamily: sdiA regulatory protein

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 9 LW 10

RESULT 15

A29169
phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 31-Oct-1997
C:Accession: A29169
R:Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.
Eur. J. Biochem. 53, 91-97, 1975
A:Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.
A:Reference number: A94661
A:Accession: A29169
A:Molecule type: protein
A:Residues: 1-12 <DUT>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase; pyroglutamic acid
F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
||
Db 9 LW 10

Search completed: February 12, 2003, 11:15:30
Job time : 5.41667 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 11:11:31 ; Search time 2.70833 Seconds
(without alignments)
76.572 Million cell updates/sec

Title: US-09-403-440A-1
Perfect score: 23
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 1520

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	69.6	6	1 E101_LITRU	P82096 litoria rub
2	16	69.6	24	1 RAN_XENLA	P52301 xenopus lae
3	15	65.2	9	1 LITR_PHYRO	P08946 phyllomedus
4	15	65.2	10	1 APE_CAPGI	P80474 capnocytoph
5	15	65.2	11	1 LPW_TETH	P05624 thermus the
6	15	65.2	17	1 PH4_PERAM	P82697 periplaneta
7	15	65.2	20	1 A1BG_EQUAS	P39090 equus asinu
8	15	65.2	21	1 NDK_CANAL	Q9ur66 candida alb
9	15	65.2	22	1 CR31_LITSP	P56238 litoria spl
10	15	65.2	22	1 CR32_LITCE	P56239 litoria cae
11	15	65.2	22	1 CR33_LITCE	P56240 litoria cae
12	15	65.2	22	1 CR34_LITCE	P56241 litoria cae
13	15	65.2	23	1 CR41_LITCE	P56242 litoria cae
14	15	65.2	23	1 CR42_LITCE	P56243 litoria cae
15	15	65.2	23	1 CR43_LITCE	P56244 litoria cae
16	15	65.2	23	1 SODP_PICAB	P29427 picea abies
17	15	65.2	24	1 DMS6_PHYBI	P81490 phyllomedus
18	15	65.2	24	1 PCL1_PACGO	P82421 pachycondyl
19	15	65.2	24	1 PCL2_PACGO	P82422 pachycondyl
20	15	65.2	24	1 VGG_BPAL3	P08766 bacterioph
21	15	65.2	24	1 Y3KD_NEUCR	P22702 neurospora
22	15	65.2	25	1 VGJ_BPG4	P03652 bacterioph
23	14	60.9	20	1 COXA_THUOB	P80972 thunnus obe
24	14	60.9	25	1 COXC_THUOB	P80973 thunnus obe
25	14	60.9	25	1 COX1_PARVE	Q00502 paracoccus
26	13	56.5	8	1 AKHG_GRYBI	P14086 gryllus bim
27	13	56.5	8	1 AKH_LIBAU	P25418 libellula a
28	13	56.5	10	1 HTF_HELZE	P16353 heliothis z
29	13	56.5	13	1 YPNP_PHOLU	P41122 photorhabdu
30	13	56.5	14	1 LPW_RHIME	P18854 rhizobium m
31	13	56.5	14	1 PPK6_PERAM	P82693 periplaneta
32	13	56.5	17	1 PPK5_PERAM	P82617 periplaneta
33	13	56.5	21	1 BTK_ATRBI	P80163 atractaspis

ALIGNMENTS

RESULT 1

E101_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: SECRETED.
KW Amphibian skin; Amidation.
FT MOD RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
Amidation.

Query Match 69.6%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| : |
Db 1 FVPIW 5

RESULT 2

RAN_XENLA STANDARD; PRT; 24 AA.
AC P52301;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE GTP-binding nuclear protein RAN (TC4) (fragments).
GN RAN.

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=94019818; PubMed=8413630;
RA Moore M.S., Biobel G.;
RT "The GTP-binding protein Ran/TC4 is required for protein import into
RT the nucleus.";

34 13 56.5 21 1 SRTD_ATREN P13211 atractaspis
35 13 56.5 23 1 PQQA_KLEPN P27503 klebsiella
36 13 56.5 23 1 XYCI_ACIGB P46365 acinetobact
37 13 56.5 24 1 CCAA-STRTI P80436 streptomyce
38 13 56.5 25 1 LPCP_YEAST P08521 saccharomyc
39 13 56.5 25 1 Y15_BPT3 P20835 bacterioph
40 13 56.5 25 1 YCX8_ODOSI P49834 odontella s
41 12 52.2 7 1 WWA1_ACHFU P35919 achatina fu
42 12 52.2 7 1 WWA2_ACHFU P35920 achatina fu
43 12 52.2 7 1 WWA3_ACHFU P35921 achatina fu
44 12 52.2 8 1 HTF1_PERAM P04548 periplaneta
45 12 52.2 8 1 HTF2_PERAM P04549 periplaneta

```

RL Nature 365:661-663(1993).
CC -!- FUNCTION: GTP-BINDING PROTEIN INVOLVED IN NUCLEOCYTOPLASMIC
CC TRANSPORT. REQUIRED FOR THE IMPORT OF PROTEIN INTO THE NUCLEUS AND
CC ALSO FOR RNA EXPORT. INVOLVED IN CHROMATIN CONDENSATION AND
CC CONTROL OF CELL CYCLE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE RAN FAMILY IN THE RAS SUPERFAMILY.
CC HSP; PI7080; IAK2K.
DR InterPro; IPR002041; RAN.
DR PROSITE; PS01115; RAN; PARTIAL.
KW GTP-binding; Nuclear protein; Protein transport.
FT NON_TER 1
FT NON_CONS 13 14 GTP (BY SIMILARITY).
FT NP_BIND 18 22
FT NON_TER 24 24
FT SEQUENCE 24 AA; 2657 MW; B69F83236247A250 CRC64;
SQ
Query Match 69.6%; Score 16; DB 1; Length 24;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FXXLM 5
DB 13 FNVW 17
RESULT 3
LITR PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rhode's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Erspamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei."
RL FEBS Lett. 182:53-56(1985).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; S07241; S07241.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 1090 MW; 4ECC1B861ADC377 CRC64;
SQ
Query Match 65.2%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 2 LW 3
RESULT 4
APE CAPGI 1
ID APE_CARGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
SQ
Nature 365:661-663(1993).
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
RT factor."
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
CC Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1 1
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;
SQ
Query Match 65.2%; Score 15; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 LW 5
DB 5 LW 6
RESULT 5
LPW THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Thermus; Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG."
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X07744; CAA30565.1; -.
DR PIR; S03315; LFTWWE.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;
Query Match 65.2%; Score 15; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 7 LW 8

RESULT 6
PH4_PERAM
ID_NDK_CANAL STANDARD; PRT; 17 AA.
AC P82697;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide hormone 4 (Pea-VLS-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattelloidea; Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=20140865; PubMed=10676456;
RA Predel R., Eckert M., Holman G.M.;
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs
of insects.";
RL Ann. N.Y. Acad. Sci. 897:282-290 (1999).
CC -!- FUNCTION: UNKNOWN.
CC -!- MASS SPECTROMETRY: MW=1966.48; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD RES 17
SQ SEQUENCE 17 AA; 1968 MW; CAAPF57ECD8218A9 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 4 LW 5

RESULT 7
A1BG_EQUAS
ID_A1BG_EQUAS STANDARD; PRT; 20 AA.
AC P39090;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Alpha-1B-glycoprotein (Postalbumin) (Fragment).
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=91330579; PubMed=1868686;
RA Patterson S.D., Bell K., Shaw D.C.;
RT "Donkey and horse alpha 1 B-glycoprotein: partial characterization
and new alleles.";
RL Comp. Biochem. Physiol. 98B:523-528 (1991).
CC -!- FUNCTION: PLASMA GLYCOPROTEIN OF UNKNOWN FUNCTION.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
KW Immunoglobulin domain; Glycoprotein; Plasma.
FT NON TER 20
SQ SEQUENCE 20 AA; 2197 MW; 65857DFDA68EBD9F CRC64;

Query Match 65.2%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 10 LW 11

RESULT 8
NDK_CANAL
ID_NDK_CANAL STANDARD; PRT; 21 AA.
AC Q9UR66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase) (NDPK)
(Fragment).
DE (Fragment).
GN NDK1
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=96019963; PubMed=7487065;
RA Biondi R.M., Veron M., Walz K., Passeron S.;
RT "Candida albicans nucleoside-diphosphate kinase: purification and
characterization.";
RL Arch. Biochem. Biophys. 323:187-194 (1995).
CC -!- FUNCTION: MAJOR ROLE IN THE SYNTHESIS OF NUCLEOSIDE TRIPHOSPHATES
OTHER THAN ATP (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
CC -!- SUBUNIT: HOMOHEXAMER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE NDK FAMILY.
HSSP: P22887; 1LWX.
DR InterPro; IPR001564; NDK.
DR Pfam; PF00334; NDK; 1.
DR PROSITE; PS00469; NDP_KINASES; 1.
KW Transferase; Kinase; ATP-binding.
FT NON TER 1
FT ACT_SITE 4
FT NON_TER 21
SQ SEQUENCE 21 AA; 2379 MW; 9DABB3A325947001 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LW 5
Db 18 LW 19

RESULT 9
CR31_LITSP
ID_CR31_LITSP STANDARD; PRT; 22 AA.
AC P56238;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Caerin 3.1.
OS Litoria splendida (Magnificent tree frog), and
Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=30345, 39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.splendida; TISSUE=Parotoid gland;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caerins and
caeridin 1 from Litoria splendida.";

J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).

[2]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RC SPECIES=L.gilleni; TISSUE=Parotoid gland;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins and
 RT caeridins from Litoria gilleni."
 RL J. Chem. Res. 139:937-961(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2382; METHOD=FAB.
 CC Antibiotic; Amphibian skin; Amidation.
 KW MOD RES 22 22
 FT SEQUENCE 22 AA; 2385 MW; 1D4411E29D43739 CRC64;
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 Db 2 LW 3

RESULT 10
 CR32_LITCE
 ID CR32_LITCE STANDARD; PRT; 22 AA.
 AC P56239;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.2.
 OS Litoria caerulea (Green tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Pelodyadinae; Litoria.
 CC NCBI_TaxID=30344;
 [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT Litoria caerulea."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2397; METHOD=FAB.
 CC Antibiotic; Amphibian skin; Amidation.
 KW MOD RES 22 22
 FT SEQUENCE 22 AA; 2400 MW; 1D440B3829D4367C CRC64;
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 Db 2 LW 3

RESULT 11
 CR33_LITCE
 ID CR33_LITCE STANDARD; PRT; 22 AA.
 AC P56240;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Caerin 3.3.
 OS Litoria caerulea (Green tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Pelodyadinae; Litoria.
 CC NCBI_TaxID=30344;
 [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT Litoria caerulea."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2424; METHOD=FAB.
 CC Antibiotic; Amphibian skin; Amidation.
 KW MOD RES 22 22
 FT SEQUENCE 22 AA; 2427 MW; 1D440B2200D4367C CRC64;
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 Db 2 LW 3

RESULT 12
 CR34_LITCE
 ID CR34_LITCE STANDARD; PRT; 22 AA.
 AC P56241;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.4.
 OS Litoria caerulea (Green tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Pelodyadinae; Litoria.
 CC NCBI_TaxID=30344;
 [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT Litoria caerulea."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW=2452; METHOD=FAB.
 CC Antibiotic; Amphibian skin; Amidation.
 KW MOD RES 22 22
 FT SEQUENCE 22 AA; 2455 MW; 3AB40B2200D43663 CRC64;
 SQ

Query Match 65.2%; Score 15; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 Db 2 LW 3

RESULT 13
 CR41_LITCE

ID CR41_LITCE STANDARD; PRT; 23 AA.
 AC P56242;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 4.1.
 OS Litoria caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea".
 RL J. Chem. Res. 138:910-936(1993).
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -!- MASS SPECTROMETRY: MW=2326; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD RES 23 23 AMIDATION.
 SQ SEQUENCE 23 AA; 2329 MW; 83BFD80B6ADDC87 CRC64;

 Query Match 65.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 LW 5
 DB 2 LW 3

 RESULT 14
 CR42_LITCE STANDARD; PRT; 23 AA.
 AC P56243;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 4.2.
 OS Litoria caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea".
 RL J. Chem. Res. 138:910-936(1993).
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -!- MASS SPECTROMETRY: MW=2340; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD RES 23 23 AMIDATION.
 SQ SEQUENCE 23 AA; 2343 MW; 83BFD8516ADDC87 CRC64;

 Query Match 65.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 LW 5
 DB 2 LW 3

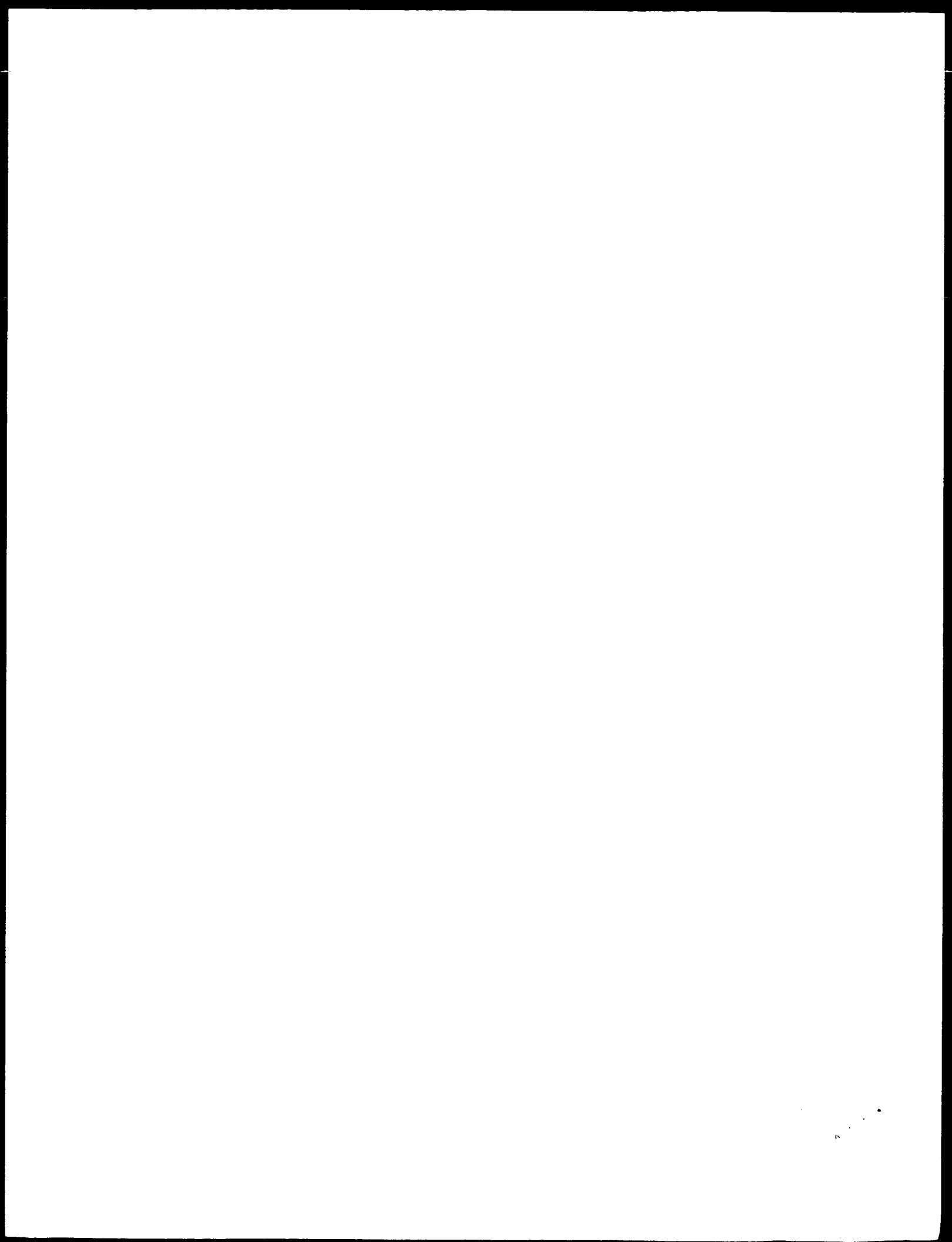
Db 2 LW 3

 RESULT 15
 CR43_LITCE STANDARD; PRT; 23 AA.
 AC P56244;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 4.3.
 OS Litoria caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 Litoria caerulea".
 RL J. Chem. Res. 138:910-936(1993).
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 GLANDS.
 CC -!- MASS SPECTROMETRY: MW=2353; METHOD=FAB.
 KW Antibiotic; Amphibian skin; Amidation.
 FT MOD RES 23 23 AMIDATION.
 SQ SEQUENCE 23 AA; 2356 MW; B98FDD80B6ADDC9D CRC64;

 Query Match 65.2%; Score 15; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 DB 2 LW 3

Search completed: February 12, 2003, 11:14:05
 Job time : 3.70833 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:02 ; Search time 9.79167 Seconds
(without alignments)
105.216 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23 FXXLW 5

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 9297

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	87.0	22	13 Q9W6D7	Q9W6D7 gallus gall
2	20	87.0	25	4 Q9NP68	Q9NP68 homo sapien
3	20	87.0	25	13 Q9UWV3	Q9UWV3 brachydanio
4	19	82.6	21	11 Q61943	Q61943 mus musculus
5	18	78.3	23	4 Q9BYM6	Q9BYM6 homo sapien
6	17	73.9	12	2 Q53579	Q53579 rhodobacter
7	17	73.9	15	2 Q53580	Q53580 rhodobacter
8	17	73.9	16	11 Q9QW76	Q9QW76 mus sp. hom
9	17	73.9	20	11 Q35353	Q35353 rattus norv
10	17	73.9	20	12 Q66548	Q66548 human herpe
11	16	69.6	17	15 Q72017	Q72017 human immun
12	16	69.6	25	2 Q9S0U6	Q9S0U6 shigella so
13	16	69.6	25	16 P72429	P72429 salmonella
14	15	65.2	8	2 Q85406	Q85406 coxiella bu
15	15	65.2	9	4 Q95953	Q95953 homo sapien
16	15	65.2	9	9 Q38366	Q38366 bacterioph

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17 15 65.2 10 4 Q8WTT4
18 15 65.2 10 8 Q8SHF6
19 15 65.2 10 11 Q9ESU5
20 15 65.2 11 2 Q47602
21 15 65.2 11 4 Q9UCR1
22 15 65.2 11 4 Q9UB69
23 15 65.2 11 6 Q9GL48
24 15 65.2 11 7 Q77895
25 15 65.2 11 7 Q77896
26 15 65.2 11 8 Q9G649
27 15 65.2 12 11 Q63579
28 15 65.2 12 15 Q98240
29 15 65.2 13 2 Q49230
30 15 65.2 13 8 Q9XLI2
31 15 65.2 14 2 Q9R782
32 15 65.2 14 4 Q99902
33 15 65.2 14 6 Q77538
34 15 65.2 14 8 Q9MT61
35 15 65.2 14 8 Q9MRV1
36 15 65.2 14 8 Q9MRV4
37 15 65.2 14 8 Q9MT8
38 15 65.2 14 11 Q9JHK8
39 15 65.2 14 15 Q98Y97
40 15 65.2 15 4 Q96RX1
41 15 65.2 16 11 Q920J2
42 15 65.2 16 13 Q8UUF8
43 15 65.2 16 13 Q8UUF7
44 15 65.2 16 13 Q8UUF6
45 15 65.2 16 13 Q8UUF5

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ALIGNMENTS

RESULT 1

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Q9W6D7 ID Q9W6D7 PRELIMINARY; PRT; 22 AA.
AC Q9W6D7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hydroxyindole-O-methyltransferase isoform A (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99067015; PubMed=9851690;
RA Grechez-Cassiau A., Bernard M., Ladjali K., Rodriguez I.R., Voisin P.;
RT "Structural analysis of the chicken hydroxyindole-O-methyltransferase
gene.";
RL Eur. J. Biochem. 258:44-52(1998).
DR EMBL; AF116455; AAD23444.1; -.
KW Methyltransferase; Transferase.
FT NON TER 1
SQ SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;

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Query Match 87.0%; Score 20; DB 13; Length 22;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 12 FADLW 16

RESULT 2

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Q9NP68 ID Q9NP68 PRELIMINARY; PRT; 25 AA.
AC Q9NP68;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Tumor suppressor p53 (Fragment).
GN TP53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thompson-Hehir J., Davies M.P.A., Green J.A., Halliwell N.,
RA Joyce K.A., Salisbury J., Sibson D.R., Vergote I., Walker C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF209136; AAF36362.1; -
DR EMBL; AF209128; AAF36354.1; -
DR EMBL; AF209129; AAF36355.1; -
DR EMBL; AF209130; AAF36356.1; -
DR EMBL; AF209131; AAF36357.1; -
DR EMBL; AF209132; AAF36358.1; -
DR EMBL; AF209133; AAF36359.1; -
DR EMBL; AF209134; AAF36360.1; -
DR EMBL; AF209135; AAF36361.1; -
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
FT NON TER 25
SQ SEQUENCE 25 AA; 2890 MW; D7FA272EBFAB9798 CRC64;

Query Match 87.0%; Score 20; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 19 FSDLW 23

RESULT 3
Q8UUVW3 PRELIMINARY; PRT; 25 AA.
AC Q8UUVW3.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AMPA receptor subunit 2 (Fragment).
GN GLUR2B.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
RA "O/R RNA editing of the AMPA receptor subunit GluR2 transcript evolves
RA no later than the appearance of cartilaginous fishes.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350049; AAL57191.1; -
DR InterPro; IPR001320; Ion_glu_receptor.
DR ProDom; PD000500; Ion_glu_receptor; 1.
FT NON TER 1
FT NON TER 25
FT NON TER 25
SQ SEQUENCE 25 AA; 2837 MW; 9EB8AA36B50DB17E CRC64;

Query Match 87.0%; Score 20; DB 13; Length 25;
Best Local Similarity 60.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 *FXXLW 5
Db 6 FNSLW 10

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RESULT 4
Q61943 PRELIMINARY; PRT; 21 AA.
ID Q61943.
AC Q61943.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nicotinic acetylcholine receptor beta 2-subunit protein
DE (Fragment).
GN CHRN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D9A2;
RX MEDLINE=96164254; PubMed=8596650;
RA Bessis A., Salmon A.M., Zoli M., Le Novere N., Picciotto M.,
RA Changeux J.P.;
RA "Promoter elements conferring neuron-specific expression of the beta
RA 2-subunit of the neuronal nicotinic acetylcholine receptor studied in
RA vitro and in transgenic mice.";
RL Neuroscience 69:807-819 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D9A2;
RA Bessis A.E.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X82655; CAA57978.1; -
DR MGD; MGI:87891; Chrn2.
KW Receptor.
FT NON TER 21
FT NON TER 21
SQ SEQUENCE 21 AA; 2351 MW; 28E57E2BC2BC67FA CRC64;

Query Match 82.6%; Score 19; DB 11; Length 21;
Best Local Similarity 60.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 14 FGLW 18

RESULT 5
Q9BYM6 PRELIMINARY; PRT; 23 AA.
ID Q9BYM6.
AC Q9BYM6.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE DSRNA adenosine deaminase (Fragment).
GN DSRAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Deblandre G., Marinx O., Nols C., Defrance P., Berr P., Huez G.;
RA Caput D.;
RA "The gene coding for the interferon-inducible human dsRNA adenosine
RA deaminase is transcribed into several messengers specifying different
RA proteins.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X98560; CAA67171.1; -
FT NON TER 23
FT NON TER 23
SQ SEQUENCE 23 AA; 2543 MW; CF29179B7DFC1395 CRC64;

Query Match 78.3%; Score 18; DB 4; Length 23;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FXXLW 5
Db 19 FFAVW 23

RESULT 6
Q53579
ID Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUF.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa
mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97551; AAC60405.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6E8A8A70532B CRC64;

Query Match 73.9%; Score 17; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 4 FYKIW 8

RESULT 7
Q53580
ID Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUF.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa
mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97552; AAC60406.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 4 FYKIW 8

RESULT 8

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Q9QW76
ID Q9QW76 PRELIMINARY; PRT; 16 AA.
AC Q9QW76;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Homeobox GSH-3 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92073356; PubMed=1683707;
RA Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.;
RT "Identification of 10 murine homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 2183 MW; BE902130A4525041 CRC64;

Query Match 73.9%; Score 17; DB 11; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 12 FKKMW 16

RESULT 9
Q35353
ID Q35353 PRELIMINARY; PRT; 20 AA.
AC Q35353;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Guanine nucleotide-binding protein beta subunit 4 (Transducin beta
chain 4) (Fragment).
GN GNB4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND DISTRIBUTION IN BRAIN.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=98283588; PubMed=9622245;
RA Betty M., Harnish S.W., Rhodes K.J., Cockett M.I.;
RT "Distribution of heterotrimeric G-protein beta and gamma subunits in
the rat brain.";
RL Neuroscience 85:475-486(1998).
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE
SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE
GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
EFFECTOR INTERACTION.
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE BRAIN. HIGHEST LEVELS
CC -1- FOUND IN THE HIPPOCAMPUS AND LAYERS V AND VI OF THE NEOCORTX.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF022085; AAB82552.1; -.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD REPEATS_1; PARTIAL.
DR PROSITE; PS00082; WD REPEATS_2; 1.
DR PROSITE; PS50294; WD REPEATS_REGION; 1.
DR Transducer; Repeat; WD repeat; Multigene family.
FT NON_TER 1 1
FT REPEAT <1 20 WD7.

```

SQ SEQUENCE 20 AA; 2242 MW; C143688295AE0BE0 CRC64;

Query Match 73.9%; Score 17; DB 11; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 Db 15 FLRIW 19

RESULT 10

Q66548 PRELIMINARY; PRT; 20 AA.
 AC Q66548;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EBV B95-8 Cl(g) DNA with antigen-coding ORF (Fragment).
 OS Human herpesvirus 4 (Epstein-Barr virus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Lymphocryptovirus.
 NCBI_TaxID=10376;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=88217505; PubMed=2835748;
 RA Walls D., Perricaudet M., Gannon F.;
 RT "The analysis of EBV proteins which are antigenic in vivo."
 RL Nucleic Acids Res. 16:2859-2872(1988).
 DR EMBL; X07531; CAA30406.1; -.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2576 MW; 05F877676B235F95 CRC64;

Query Match 73.9%; Score 17; DB 12; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.4e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 Db 11 FRFIW 15

RESULT 11

Q72017 PRELIMINARY; PRT; 17 AA.
 AC Q72017;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Env protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Michael N.L.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U24486; AAA79676.1; -.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 2072 MW; BOAEB4D30DE21302 CRC64;

Query Match 69.6%; Score 16; DB 15; Length 17;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 Db 10 YQHLW 14

RESULT 12

Q9S0U6 PRELIMINARY; PRT; 25 AA.
 ID Q9S0U6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF10S (Fragment).
 OS Shigella sonnei.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HW383;
 RX MEDLINE=20248365; PubMed=10789503;
 RA Chida T., Okamura N., Ohtani K., Yoshida Y., Arakawa E., Watanabe H.;
 RT "The complete DNA sequence of the O antigen gene region of Plesiomonas
 shigelloides serotype O17 which is identical to Shigella sonnei form
 I antigen."
 RL Microbiol. Immunol. 44:161-172(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HW383;
 RX MEDLINE=99036814; PubMed=9817819;
 RA Hough H.H., Venkatesan M.M.;
 RT "Genetic analysis of Shigella sonnei form I antigen: identification of
 a novel 18630 as an essential element for the form I antigen
 RT expression."
 RL Microb. Pathog. 25:165-173(1998).
 DR EMBL; AB028134; BAA85070.1; -.
 FT NON TER 25
 SQ SEQUENCE 25 AA; 2726 MW; A6CC5D24211CDAAD CRC64;

Query Match 69.6%; Score 16; DB 2; Length 25;
 Best Local Similarity 40.0%; Pred. No. 4.8e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXLW 5
 Db 10 FGTFW 14

RESULT 13

P72429 PRELIMINARY; PRT; 25 AA.
 ID P72429;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE TAP/REPC (Replication of plasmid).
 GN TAP/REPC OR TAP OR PSLT005.
 OS Salmonella enteritidis.
 OS Salmonella enterica subsp. enterica serovar Choleraesuis, and
 OS Salmonella typhimurium.
 OG Plasmid virulence, Plasmid 50k virulence, and Plasmid pSLT.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=592, 119912, 602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.enteritidis; STRAIN=82139; PLASMID=VIRULENCE;
 RX MEDLINE=9725449; PubMed=9099859;
 RA Rodriguez-Pena J.M., Buisan M., Ibanez M., Rotger R.;
 RT "Genetic map of the virulence plasmid of Salmonella enteritidis and
 RT nucleotide sequence of its replicons."
 RL Gene 188:53-61(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.enterica subsp. enterica serovar Choleraesuis; STRAIN=RF-1;
 RC PLASMID=50K VIRULENCE;
 RA Okada N., Haneda T.;
 RT "50 kb virulence plasmid of Salmonella enterica serovar
 RT Choleraesuis.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC PLASMID=PSLT;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; U64797; AAB53038.1; -.
 DR EMBL; AB040415; BAB20531.1; -.
 DR EMBL; AE006471; AAL23447.1; -.
 KW Plasmid; Complete proteome.
 SQ SEQUENCE 25 AA; 3008 MW; B21F596B6DEFABE7 CRC64;

Query Match 69.6%; Score 16; DB 16; Length 25;
 Best Local Similarity 40.0%; Pred. No. 4.8e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 : ||
 Db 7 YLFLW 11

RESULT 14

O85406
 ID O85406 PRELIMINARY; PRT; 8 AA.
 AC O85406;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 OS Coccidia burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC Coccidia group; Coccidia.
 OX NCBI_TaxID=777;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE I;
 RX MEDLINE=98348442; PubMed=9683477;
 RA Willems H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 RT Coccidia burnetii.";
 RL J. Bacteriol. 180:3816-3822(1998).
 DR EMBL; AF064963; AAD09947.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 993 MW; 045B5AA45372727 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 : ||
 Db 3 LW 4

RESULT 15

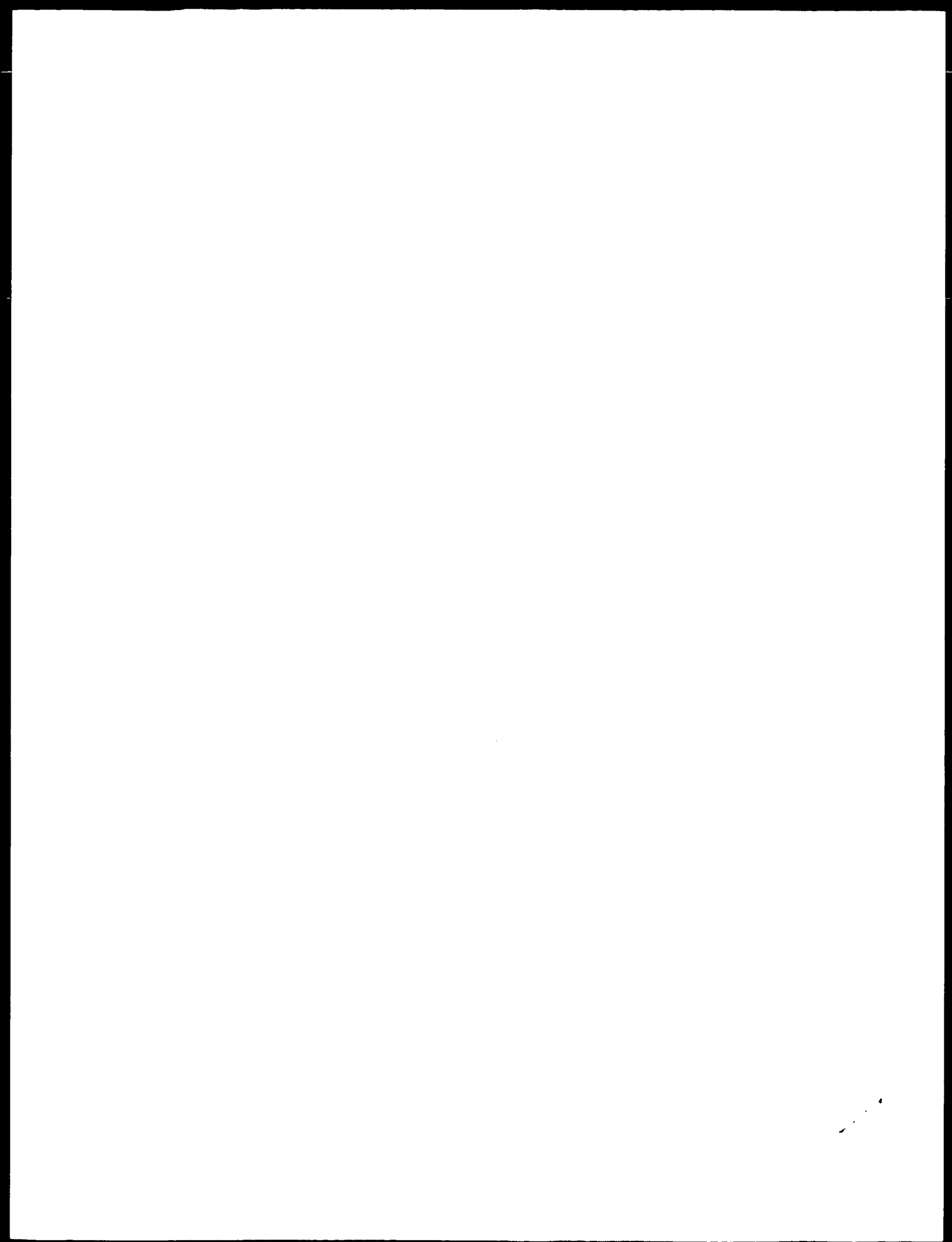
O95953
 ID O95953 PRELIMINARY; PRT; 9 AA.
 AC O95953;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Galactocerebrosidase (EC 3.2.1.46) (Fragment).
 GN GALT.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Lulli L., Torchiana E., Finocchiaro G.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U77631; AAD15626.1; -.
 KW Glycosidase; Hydrolase.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2AAD2C2C699C8 CRC64;

Query Match 65.2%; Score 15; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LW 5
 : ||
 Db 8 LW 9

Search completed: February 12, 2003, 11:14:58
 Job time : 10.7917 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:10:52 ; Search time 12.5 Seconds
(without alignments)
53.300 Million cell updates/sec

Title: US-09-403-440A-1
Perfect score: 23
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 320064

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*

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23: /SID52/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	15	21 AAB29164	Peptide #8. Unide
2	20	87.0	5	20 AAY33038	Carbohydrate anti
3	20	87.0	5	21 AAB07280	Motif binding to a
4	20	87.0	6	17 AAR89913	p53/MDM2 binding i
5	20	87.0	6	17 AAR89915	p53 minimal MDM2 b
6	20	87.0	6	18 AAW13606	p53 protein amino
7	20	87.0	6	21 AAB17074	Mdm/hdm antagonist
8	20	87.0	6	23 ABB73169	Mdm/hdm antagonist
9	20	87.0	7	17 AAR89921	Antibody DO-1 epit
10	20	87.0	7	17 AAR89925	p53 binding site k

11	20	87.0	7	20 AAW94141	FG loop sequence o
12	20	87.0	7	21 AAY57789	TRAM-interaction m
13	20	87.0	7	23 ABB94392	Ubiquitin binding
14	20	87.0	8	21 AAB09130	Hepatitis GB virus
15	20	87.0	8	22 AAB62220	Glycine max homogl
16	20	87.0	9	19 AAW37199	Human oncogenic pr
17	20	87.0	9	19 AAW46349	Amino acid sequenc
18	20	87.0	9	19 AAW46350	Amino acid sequenc
19	20	87.0	9	19 AAW46351	Amino acid sequenc
20	20	87.0	9	21 AAB34807	Human secreted pro
21	20	87.0	10	17 AAR89917	Human p53 MDM2-con
22	20	87.0	10	17 AAR89918	Mouse p53 MDM2-con
23	20	87.0	10	18 AAW13605	p53 protein amino
24	20	87.0	10	19 AAW37198	Human oncogenic pr
25	20	87.0	11	18 AAW11231	Peptide A, used in
26	20	87.0	11	22 AAU26842	Human Leukocyte An
27	20	87.0	11	22 AAU27152	Human Leukocyte An
28	20	87.0	11	23 AAW52269	Miniature protein
29	20	87.0	12	19 AAW37181	Human p53 wild-typ
30	20	87.0	12	19 AAW37188	Human oncogenic pr
31	20	87.0	12	19 AAW37189	Human oncogenic pr
32	20	87.0	12	21 AAB17075	Mdm/hdm antagonist
33	20	87.0	12	21 AAB17076	Mdm/hdm antagonist
34	20	87.0	12	21 AAB17087	Mdm/hdm antagonist
35	20	87.0	12	21 AAB17088	Mdm/hdm antagonist
36	20	87.0	12	22 AAB86005	DCM-associated pep
37	20	87.0	12	23 ABB73170	Mdm/hdm antagonist
38	20	87.0	12	23 ABB73171	Mdm/hdm antagonist
39	20	87.0	12	23 ABB73182	Mdm/hdm antagonist
40	20	87.0	12	23 ABB73183	Mdm/hdm antagonist
41	20	87.0	13	21 AAY57799	TRAM-interaction m
42	20	87.0	13	22 AAB86006	DCM-associated pep
43	20	87.0	14	22 AAG98212	Human SNP associat
44	20	87.0	14	22 AAB86012	DCM-associated pep
45	20	87.0	14	22 AAB86020	DCM autoantibody-a

ALIGNMENTS

RESULT 1
AAB29164
ID AAB29164 standard; Peptide; 15 AA.
XX AAB29164;
XX AC AAB29164;
XX DT 02-FEB-2001 (first entry)
XX DE Peptide #8.
XX DE Fork head associated; FHA; domain; transcriptional control;
XX KW DNA replication; DNA repair; cell cycle control.
XX OS Unidentified.
XX PN WO200057184-A2.
XX PD 28-SEP-2000.
XX PF 17-MAR-2000; 2000WO-GB01024.
XX PR 19-MAR-1999; 99GB-0006432.
XX PR 28-JUN-1999; 99GB-0015075.
XX PA (KUDO-) KUDOS PHARM LTD.
XX PI Jackson SP, Durocher D;
XX DR WPI; 2000-664872/64.
XX PT Assays and screening methods based on direct interaction between FHA
PT domains and phosphopeptides, useful for characterizing binding and to
PT identify binding partners and modulators of FHA domain-phosphopeptide

PT binding -

XX Disclosure; Fig 2; 92pp; English.

XX The present invention relates to assays and screening methods based on a direct interaction between fork head associated (FHA) domains and phosphorylated polypeptides, for characterizing the binding of these molecules. FHA peptides may be useful for treating medical conditions associated with defects in transcriptional control, DNA replication, DNA repair, cell cycle control or other cellular processes. The method may provide valuable insights into checkpoint signalling, has important implications for the functions of other FHA domain-containing proteins and provides basis for new lines of therapy. The present sequence is a peptide used in the present invention.

XX Sequence 15 AA;

SQ Query Match 91.3%; Score 21; DB 21; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FXXLW 5
| | |
Db 9 FSALW 13

RESULT 2

AAV33038

ID AAY33038 standard; peptide; 5 AA.

XX AC AAY33038;

XX 03-NOV-1999 (first entry)

XX Carbohydrate antigen peptide mimotope 11.

XX Mimotope; antigen; carbohydrate; antibody; mimic; vaccine; adjuvant;
tumour immunity; cancer therapy; antibacterial; immune response;
immunogenicity; anti-idiotype; T cell response manipulation.

XX Synthetic.

XX WO9940433-A1.

XX 12-AUG-1999.

XX 04-FEB-1999; 99WO-US02405.

XX 04-FEB-1998; 98US-0073690.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Kieber-Emmons T;

XX WPI; 1999-527317/44.

XX Peptides and recombinant antibody mimics of carbohydrate antigens,
used for, e.g. treatment of cancer and infection

XX Claim 21; Page 72; 88pp; English.

XX This invention describes a novel method for preparing a peptide or recombinant antibody, which mimics an antigenic carbohydrate. The peptides and recombinant antibodies prepared to mimic antigenic carbohydrates can be used to enhance binding of anti-antigenic carbohydrate antibodies to the antigenic carbohydrate, e.g. as vaccine adjuvants. The peptides can be used to inhibit binding of a ligand to a receptor, which is an antigenic carbohydrate. The methods are used to prepare the peptides and antigenic antibodies, which mimic the antigenic carbohydrates. Carbohydrate-conjugate vaccines could be used in tumour immunity and cancer therapy. The peptides and antibodies can also be used as antibacterials. Peptides that mimic carbohydrate antigens can be formulated to develop a longer lasting immune response. Other advantages

CC of the peptide mimics are; (1) the chemical composition and purity of synthesized peptides can be precisely defined; (2) the immunogenicity of the peptides can be significantly enhanced by polymerization or addition of relatively small carrier molecules that reduce the total amount of antigen required for immunization; (3) peptide synthesis may be more practical than synthesis of carbohydrate-protein conjugates or the production of anti-idiotypes; (4) peptide mimicking sequences can be engineered into DNA plasmids for DNA vaccination to further manipulate T cell responses. AAY33028-Y33087 represent the carbohydrate antigen peptide mimotopes described in the invention.

XX Sequence 5 AA;

SQ Query Match 87.0%; Score 20; DB 20; Length 5;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

Oy 1 FXXLW 5
| | |
Db 1 FSLLW 5

RESULT 3

AAAB07280

ID AAB07280 standard; peptide; 5 AA.

XX AC AAB07280;

XX 17-OCT-2000 (first entry)

XX Motif binding to anti-Lewis antigen antibody BR55-2.

XX Human; peptido-mimetic; tumour metastasis; E-selectin;
adhesion molecule; Lewis antigen; anti-adhesion therapy.

XX Unidentified.

XX WO200027420-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US26277.

XX 06-NOV-1998; 98US-0107478.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
(UYPE-) UNIV PENNSYLVANIA.

XX Blaszczyk-Thurin M, Kieber-Emmons T;

XX WPI; 2000-376309/32.

XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating inflammation, metastasis and angiogenesis -

XX Example 5; Page 37; 107pp; English.

XX Tumour metastasis requires detachment of malignant cells from the primary tumour, penetration of blood or lymph vessels and attachment to the endothelium of distant organs, ultimately resulting in the formation of new tumours. The selectin family of adhesion molecules is implicated in this process. E-selectin is a calcium-dependent molecule expressed by activated vascular endothelium. E-selectins bind to glycoconjugates carrying a terminal tetrasaccharide Lewis antigen, which are found on tumour cell surfaces. One such Lewis antigen is Lewis X (LeX). The binding of selectin molecules to their ligands is thought to be an important step in metastasis. Therefore, inhibition of E-selectin-dependent carbohydrate-mediated interactions is thought to be a target for anti-cancer therapy. The present sequence is a non planar-X planar type motif. This motif is thought to bind to anti-LeX antibody BR55-2. BR55-2 is a peptido-mimetic of E-selectins. Peptides that block E-selectin-LeX binding and therefore adhesion of tumour cells and leukocytes to endothelial cells inhibit metastasis.


```

XX SQ Sequence 5 AA;
Query Match 87.0%; Score 20; DB 21; Length 5;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 1 FSLWL 5

RESULT 4
AAR89913
ID AAR89913 standard; peptide; 6 AA.
XX AC AAR89913;
XX DT 10-SEP-1996 (first entry)
XX DE p53/MDM2 binding inhibitor #3.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picksley SM;
XX DR WPI; 1996-105905/11.
XX PT New cpds. which interfere with binding of MDM2 and p53 - used to
XX PT develop prods. for use in the diagnosis and treatment of cancer and
XX PS other malignancies
XX PS Claim 4; Page 29; 46pp; English.
XX CC New peptides of the invention which interfere with the binding of the
XX CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
XX CC the peptide sequences AAR89911-3 which form part of the p53 protein
XX CC binding motif between amino acids 16-33 (AAR89914). The peptides were
XX CC identified by modifying the p53 consensus binding sequence by
XX CC substitution of an Alanine at each pos. and identifying which amino
XX CC acid changes altered binding to expressed MDM2. The peptides and
XX CC methods of identifying similar inhibitory peptides can be used to
XX CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSDLW 6

RESULT 5
AAR89915
ID AAR89915 standard; peptide; 6 AA.
XX AC AAR89915;
XX DT 10-SEP-1996 (first entry)
XX DE p53 minimal MDM2 binding site #1.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picksley SM;
XX DR WPI; 1996-105905/11.
XX PT New cpds. which interfere with binding of MDM2 and p53 - used to
XX PT develop prods. for use in the diagnosis and treatment of cancer and
XX PS other malignancies
XX PS Disclosure; Page 15; 46pp; English.
XX CC This is the sequence of the p53 tumour suppressor protein minimal MDM2
XX CC oncogene protein binding site. The sequence is used to generate peptides
XX CC binding motif between amino acids 16-33 (AAR89914). The peptides were
XX CC identified by modifying the p53 consensus binding sequence by
XX CC substitution of an Alanine at each pos. and identifying which amino
XX CC acid changes altered binding to expressed MDM2. The peptides and
XX CC methods of identifying similar inhibitory peptides can be used to
XX CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSGLW 6

RESULT 6
AAW13606
ID AAW13606 standard; peptide; 6 AA.
XX AC AAW13606;
XX DT 16-JAN-1998 (first entry)
XX DE p53 protein amino acids 18-23.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW restenosis.
XX OS Homo sapiens.
XX PN WO9709343-A2.
XX XX

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AC AAR89915;
XX DT 10-SEP-1996 (first entry)
XX DE p53 minimal MDM2 binding site #1.
XX KW Interference; binding; p53; tumour suppressor; MDM2; oncogene; cancer;
XX KW inhibition; diagnosis; treatment; malignancy; consensus.
XX OS Synthetic.
XX PN WO9602642-A1.
XX PD 01-FEB-1996.
XX PF 20-JUL-1995; 95WO-GB01719.
XX PR 19-APR-1995; 95US-0424957.
XX PR 20-JUL-1994; 94US-0277660.
XX PA (UYDU-) UNIV DUNDEE.
XX PI Lane DP, Picksley SM;
XX DR WPI; 1996-105905/11.
XX PT New cpds. which interfere with binding of MDM2 and p53 - used to
XX PT develop prods. for use in the diagnosis and treatment of cancer and
XX PS other malignancies
XX PS Disclosure; Page 15; 46pp; English.
XX CC This is the sequence of the p53 tumour suppressor protein minimal MDM2
XX CC oncogene protein binding site. The sequence is used to generate peptides
XX CC binding motif between amino acids 16-33 (AAR89914). The peptides were
XX CC identified by modifying the p53 consensus binding sequence by
XX CC substitution of an Alanine at each pos. and identifying which amino
XX CC acid changes altered binding to expressed MDM2. The peptides and
XX CC methods of identifying similar inhibitory peptides can be used to
XX CC diagnose and treat e.g. cancer and other malignancies.
XX SQ Sequence 6 AA;
Query Match 87.0%; Score 20; DB 17; Length 6;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
   |  |  |
Db 2 FSGLW 6

RESULT 6
AAW13606
ID AAW13606 standard; peptide; 6 AA.
XX AC AAW13606;
XX DT 16-JAN-1998 (first entry)
XX DE p53 protein amino acids 18-23.
XX KW Mouse; Mdm2; murine double minute; phosphoprotein; binding; modulation;
XX KW tumour suppressor; p53; oncogene; cell cycle arrest; p107; antagonist;
XX KW inhibition; transcription factor; adenocarcinoma; colon; cancer; breast;
XX KW lung; stomach; myeloid leukaemia; lymphoma; hyperproliferative;
XX KW restenosis.
XX OS Homo sapiens.
XX PN WO9709343-A2.
XX XX

```

PD 13-MAR-1997.
 XX
 PD 02-SEP-1996; 96WO-FR01340.
 XX
 PD 04-SEP-1995; 95FR-0010331.
 XX
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 PA (RHON) RHONE POULENC RORER SA.
 XX
 PI Dubs-Poterszman M, Tocque B, Waslylyk B;
 XX
 DR WPI; 1997-192837/17.
 XX
 PT Treating cancer with antagonist of oncogenic activity of protein
 PT Mdm2 - or nucleic acid encoding an antagonist, also viral vectors
 PT contg. this nucleic acid
 XX
 PS Claim 4; Page -; 43pp; French.
 XX
 CC The peptides AAW13602-6 represent peptide fragments derived from the
 CC wild type human p53 protein. This peptide corresponds to amino acids
 CC 18-23 of the p53 sequence. The peptides are claimed peptides which are
 CC able to bind the N-terminal amino acids (1-134) of the murine double
 CC minute-2 (mdm2) protein (AAW13600). Mdm2 protein is a 90 kD
 CC phosphoprotein which binds and modulates the activity of the tumour
 CC suppressor protein p53. It has now been shown that the mdm2 protein
 CC itself has oncogenic properties, especially in a p53-null background.
 CC Mdm2 is observed to unblock cell cycle arrest in G1 caused by
 CC over-expression of the p107 protein. The p53 peptides are examples of
 CC antagonists of the invention which are able to inhibit the oncogenic
 CC activity of mdm2. The antagonists are used to treat e.g. adenocarcinoma
 CC of the colon; cancer of the breast, lung or stomach; myeloid leukaemia; B
 CC cell lymphoma, or other hyperproliferative conditions such as
 CC restenosis. Note: this sequence is not given in the specification but is
 CC constructed from the wild type human p53 sequence.
 XX
 SQ Sequence 6 AA;
 Query Match 87.0%; Score 20; DB 18; Length 6;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXLW 5
 | | |
 Db 2 FSDLW 6
 RESULT 7
 AAB17074
 ID AAB17074 standard; Peptide; 6 AA.
 XX
 AC AAB17074;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Mdm/hdm antagonist peptide sequence SEQ ID NO:130.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX

PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 39; Page 240; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, (L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 87.0%; Score 20; DB 21; Length 6;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXLW 5
 | | |
 Db 2 FSDLW 6
 RESULT 8
 ABB73169
 ID ABB73169 standard; Peptide; 6 AA.
 XX
 AC ABB73169;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Mdm/hdm antagonist peptide SEQ ID NO:130.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183525-A2.
 XX

XX New peptides of the invention which interfere with the binding of the
 CC p53 tumour suppressor protein and the MDM2 oncogene protein contain
 CC the peptide sequences AAR8911-3 which form part of the p53 protein
 CC binding motif between amino acids 16-33 (AAR8914). Peptides contg.
 CC these sequence were identified by immobilising a library of peptides (15
 CC amino acids long) covering the mouse or human p53 protein and adding an
 CC extract contg. expressed MDM2 protein. This sequence represent the key
 CC amino acids in the p53 binding site required for mouse MDM2 binding.
 CC The peptides and methods of identifying similar inhibitory peptides can
 CC be used to diagnose and treat e.g. cancer and other malignancies.
 XX SQ Sequence 7 AA;

Query Match 87.0%; Score 20; DB 17; Length 7;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 | | |
 DB 3 FSDLW 7

RESULT 11
 AAW94141
 ID AAW94141 standard; peptide; 7 AA.
 AC AAW94141;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE FG loop sequence of ubiquitin-binding monobody clone 213.
 XX
 KW Fibronectin type III; Fn3; monobody; beta-strand domain; loop region;
 KW specific binding partner; SBP; catalysis; LRS; ubiquitin.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN WO9856915-A2.
 XX
 PD 17-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12099.
 XX
 PR 12-JUN-1997; 97US-0049410.
 XX
 PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
 XX
 PI Koide S;
 XX
 DR WPI; 1999-060331/05.
 XX
 PT Production of antibody compounds, particularly catalytic antibodies
 PT - using a fibronectin type III molecular scaffolding comprising
 PT beta-strand domain sequences and modified in one or more loop
 PT sequences
 XX
 PS Example 10; Page 41; 96pp; English.
 XX

The invention relates to a synthetic fibronectin type III (Fn3)
 CC polypeptide monobody that comprises Fn3 beta-strand domain sequences
 CC that are linked to loop region sequences (LRSs). One or more of the loop
 CC sequences in the synthetic Fn3 vary by deletion, insertion, or
 CC replacement of at least 2 amino acids from the corresponding LRS in
 CC wild-type Fn3. Host cells containing an expression vector comprising the
 CC synthetic Fn3 nucleic acid are used for the production of the Fn3
 CC monobody. The invention also provides methods of identifying the amino
 CC acid sequence of a polypeptide molecule (i) capable of binding to a
 CC specific binding partner (SBP) so as to form a polypeptide:SBP complex;
 CC (ii) capable of catalysing a chemical reaction with a catalysed rate
 CC constant Kcat, and an uncatalysed rate constant, Kuncat, such that the
 CC ratio of the Kcat/Kuncat is greater than 10. Sequences AAW94139-46
 CC represent FG loop sequences of yeast ubiquitin-binding monobodies.

XX SQ Sequence 7 AA;

Query Match 87.0%; Score 20; DB 20; Length 7;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
 | | |
 DB 1 FADLW 5

RESULT 12
 AAY57789
 ID AAY57789 standard; peptide; 7 AA.
 AC AAY57789;
 XX
 DT 20-MAR-2000 (first entry)
 XX
 DE TRAM-interaction motif derived from p53 SEQ ID NO:12.
 XX
 KW Transcriptional adaptor motif; TRAM; TRAM interaction motif; TRIM;
 KW cAMP binding protein; transcriptional regulation; cytosolic; antiviral;
 KW cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;
 KW viral disease; viral infection; cell cycle; apoptosis; growth arrest.
 XX
 OS Unidentified.
 XX
 PN WO9961608-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 26-MAY-1999; 99WO-GB01668.
 XX
 PR 26-MAY-1998; 98GB-0011303.
 PR 05-JAN-1999; 99GB-0000157.
 XX
 PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 XX
 PI O'Connor MJ, Zimmermann H;
 XX
 DR WPI; 2000-072620/06.
 XX
 PT Novel polypeptides cells useful for treating viral disease and cancer
 PS Disclosure; Page 7; 73pp; English.
 XX

The present invention describes a polypeptide comprising a
 CC transcriptional adaptor motif (TRAM) or a TRAM-interaction motif
 CC (TRIM) (I). (I) can be used for identifying compounds (II) comprising a
 CC polypeptide capable of disrupting an interaction between a TRAM sequence
 CC and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a
 CC TRIM sequence are identified by incubating, the polypeptide with (I) and
 CC determining if the polypeptide interacts with (I). Compound (II) is
 CC useful for preparing a pharmaceutical composition and for disrupting an
 CC interaction between TRAM sequence and TRIM sequence in vitro, thereby
 CC inhibiting viral transcription or cell cycle progression in mammalian
 CC cells especially cancer cell. Compounds which disrupt interaction
 CC between TRIM/TRAM containing polypeptides can be used therapeutically to
 CC prevent or treat viral diseases and tumours. The polypeptides reduce
 CC susceptibility of cells to viral infection and regulate cell cycle
 CC including apoptosis and growth arrest and can be used to produce
 CC antibodies against the TRIM or TRAM sequences. HPV types associated
 CC with high risk or low risk of cervical cancer can be distinguished
 CC based on the ability of E6 polypeptides to bind to cAMP binding protein
 CC (CBP) TRAM sequences. The present sequence represents a TRIM sequence
 CC given in the present invention.

XX SQ Sequence 7 AA;

Query Match 87.0%; Score 20; DB 21; Length 7;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;

Matches: 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
Db 1 FSDLW 5

RESULT 13

ABB94392
ID ABB94392 standard; Peptide; 7 AA.

XX AC ABB94392;

XX DT 12-JUN-2002 (first entry)

XX DE Ubiquitin binding monocbody 213 FG loop.

XX KW Fibronectin type 3; mutant; stabilising mutation; Fn3; antibody;
XX binding protein.

XX OS Unidentified.

XX PN WO200204523-A2.

XX PD 17-JAN-2002.

XX PF 11-JUL-2001; 2001WO-US21855.

XX PR 11-JUL-2000; 2000US-217474P.

XX PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX KOIDE S.

XX PI Koide S;

XX DR WPI; 2002-171708/22.

XX PT New fibronectin type III molecule comprising a stabilising mutation,
XX useful for introducing more mutations for better functions, and in a
XX wider range of applications

XX PS Example 10; Page 138; 164pp; English.

XX CC The present invention relates to fibronectin type III (Fn3) molecules
XX comprising a stabilising mutation as compared to a wild-type Fn3. Fn3 can
XX be used as a scaffold to engineer artificial binding proteins.
XX Modifications of the Fn3 scaffold that increase its stability are useful
XX in that they allow the introduction of more mutations for better
XX functions, and that these make it possible to use Fn3-based engineered
XX proteins in a wider range of applications. The present sequence is a
XX peptide described in the exemplification of the invention.

SQ Sequence 7 AA;

Query Match . 87.0%; Score 20; DB 23; Length 7;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
Db 1 FADLW 5

RESULT 14

AB09130
ID AAB09130 standard; Protein; 8 AA.

XX AC AAB09130;

XX DT 30-AUG-2000 (first entry)

XX DE Hepatitis GB virus protein sequence SEQ ID NO:252.

XX PN

KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic;
KW infection; detection; characterisation; hepatitis.

OS Hepatitis GB virus.

PN US6051374-A.

XX PD 18-APR-2000.

XX PF 07-JUN-1995; 95US-0488445.

XX PR 14-FEB-1994; 94US-0196030.

XX PR 13-MAY-1994; 94US-0242654.

XX PR 29-JUL-1994; 94US-0283314.

XX PR 23-NOV-1994; 94US-0344185.

XX PR 23-NOV-1994; 94US-0344190.

XX PR 30-JAN-1995; 95US-0377557.

XX PA (ABBO) ABBOTT LAB.

XX PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
XX Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;

XX DR WPI; 2000-338307/29.

XX PT Detecting target hepatitis GB virus nucleic acid in a test sample
XX suspected of containing HGBV comprises reacting the test sample the
XX HGBV polynucleotide probe and detecting the complex that contains
XX target HGBV

XX PS Example 9; Column 331-332; 369pp; English.

XX CC The present invention describe a method for detecting target
XX hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T)
XX suspected of containing HGBV. The method involves reacting (T) with a
XX HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and
XX which selectively hybridises to the HGBV genome or its full complement,
XX and detecting the complex that contains THN, indicating the presence of
XX target HGBV. The method is used for detecting target HGBV nucleic acid
XX in the test sample suspected of containing HGBV and for characterisation
XX of newly ascertained etiological agent of non-A, non-B, non-C, non-D and
XX non-E hepatitis causing agents collectively termed as hepatitis GB
XX virus. AAB55270 to AAB55489 and AAB08985 to AAB09480 represent nucleotide
XX and protein sequences used in the exemplification of the present
XX invention.

SQ Sequence 8 AA;

Query Match 87.0%; Score 20; DB 21; Length 8;
Best Local Similarity 60.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
Db 1 FSHLW 5

RESULT 15

AAB62220
ID AAB62220 standard; peptide; 8 AA.

XX AC AAB62220;

XX DT 11-JUN-2001 (first entry)

XX DE Glycine max homogluthathione synthetase protein region.

XX KW Soybean; glutathione-S-transferase; GST; homogluthathione synthetase;
XX HGS; beta-alanine; gamma-glutamylcysteine; herbicide.

XX OS Glycine max.

XX PN WO200121770-A2.

XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB03573.
 XX 21-SEP-1999; 99GB-0022346.
 XX (ZENE) ZENECA LTD.
 XX Andrews CJ, Jepson I, Townson JK, Edwards R, Cummins I, Skipsey M;
 XX WPI; 2001-257978/26.
 XX Novel glutathione-S-transferase and homogluthathione synthetase
 PT sequences from soybean for producing plants which are resistant and
 PT tolerant to herbicide comprising fomesafen and/or acifluorfen -
 XX
 PS Claim 9; Page 39; 64pp; English.
 XX
 CC The invention relates to new soybean glutathione-S-transferase (GST) and
 CC a homogluthathione synthetase (HGS). The HGS is capable of catalyzing the
 CC addition of beta-alanine onto gamma-glutamylcysteine. Polynucleotides
 CC encoding the proteins of the invention are useful for producing plants
 CC which are resistant and/or tolerant to a herbicide comprising fomesafen
 CC and/or acifluorfen. Methods of the invention are useful for providing
 CC plants with further desired agronomic trait, especially resistant to a
 CC herbicide, comprising glyphosate or its salt. Further desired agronomic
 CC traits include insect resistance, nematode resistance, stress tolerance,
 CC altered field, altered nutritional value, altered quality or any other
 CC desirable agronomic trait. GST or its variant is also useful as a
 CC selectable marker gene. The present sequence represents a Glycine max
 CC HGS protein fragment.
 XX
 SQ Sequence 8 AA;
 Query Match 87.0%; Score 20; DB 22; Length 8;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FXXLW 5
 Db 2 FAGLW 6

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OM protein - protein search, using sw model

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Title: US-09-403-440A-1

Perfect score: 23

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Listing first 45 summaries

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SUMMARIES

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2	20	87.0	6 10	US-09-732-384-4
3	20	87.0	6 10	US-09-732-384-5
4	20	87.0	6 12	US-10-155-059-1
5	20	87.0	7 9	US-09-903-412-36
6	20	87.0	7 10	US-09-096-749A-36
7	20	87.0	8 8	US-08-424-550B-252
8	20	87.0	9 9	US-09-884-456-8
9	20	87.0	9 9	US-09-884-456-11
10	20	87.0	9 9	US-09-884-456-14
11	20	87.0	9 10	US-09-214-371-37
12	20	87.0	9 10	US-09-214-371-38
13	20	87.0	10 10	US-09-214-371-35
14	20	87.0	10 10	US-09-214-371-36
15	20	87.0	12 10	US-09-214-371-17
16	20	87.0	12 10	US-09-214-371-24
17	20	87.0	12 10	US-09-214-371-25
18	20	87.0	15 10	US-09-950-692-6
19	20	87.0	15 10	US-09-732-384-6

20	20	87.0	16	10	US-09-214-371-39	Sequence 39, Appl
21	20	87.0	16	10	US-09-214-371-40	Sequence 40, Appl
22	20	87.0	16	10	US-09-019-679-3	Sequence 3, Appl
23	20	87.0	18	10	US-09-214-371-74	Sequence 74, Appl
24	20	87.0	19	10	US-09-214-371-1	Sequence 1, Appl
25	20	87.0	19	10	US-09-732-384-7	Sequence 7, Appl
26	20	87.0	19	12	US-10-155-059-13	Sequence 13, Appl
27	20	87.0	20	12	US-10-155-059-8	Sequence 8, Appl
28	20	87.0	20	12	US-10-155-059-10	Sequence 10, Appl
29	20	87.0	20	12	US-10-155-059-11	Sequence 11, Appl
30	20	87.0	20	12	US-10-155-059-14	Sequence 14, Appl
31	20	87.0	20	12	US-10-155-059-15	Sequence 15, Appl
32	20	87.0	20	12	US-10-155-059-16	Sequence 16, Appl
33	20	87.0	20	12	US-10-155-059-19	Sequence 19, Appl
34	20	87.0	20	12	US-10-155-059-20	Sequence 20, Appl
35	20	87.0	22	10	US-09-214-371-73	Sequence 73, Appl
36	20	87.0	22	10	US-09-864-761-35636	Sequence 35636, A
37	20	87.0	24	9	US-09-774-639-203	Sequence 203, App
38	19	82.6	5	10	US-09-214-371-2	Sequence 2, Appl
39	19	82.6	5	10	US-09-281-717-3	Sequence 3, Appl
40	19	82.6	6	12	US-10-155-059-2	Sequence 2, Appl
41	19	82.6	9	10	US-09-862-260A-9	Sequence 9, Appl
42	19	82.6	11	10	US-09-881-276-5	Sequence 5, Appl
43	19	82.6	11	10	US-09-881-276-6	Sequence 6, Appl
44	19	82.6	11	12	US-10-155-059-21	Sequence 21, Appl
45	19	82.6	13	12	US-10-155-059-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-214-371-83
; Sequence 83, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickalev, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83

Query Match 87.0%; Score 20; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 2 FSDLW 6

RESULT 2
US-09-732-384-4
; Sequence 4, Application US/09732384

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; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-4

Query Match      87.0%; Score 20; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      |  |  |
Db      2 FSDLW 6

RESULT 3
US-09-732-384-5
; Sequence 5, Application US/09732384
; Patent No. US20020132977A1
; GENERAL INFORMATION:
; APPLICANT: Yuan, Zhi-Min
; TITLE OF INVENTION: Inhibition of p53 Degradation
; FILE REFERENCE: 21508-044
; CURRENT APPLICATION NUMBER: US/09/732,384
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,816
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Protein
; OTHER INFORMATION: fragment not in inhibitory p53 polypeptide
US-09-732-384-5

Query Match      87.0%; Score 20; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      |  |  |
Db      2 FSGLW 6

RESULT 4
US-10-155-059-1
; Sequence 1, Application US/10155059
; Patent No. US20020147173A1
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE
; ANTIBODIES
```

```
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/155,059
; FILING DATE: 24-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-155-059-1

Query Match      87.0%; Score 20; DB 12; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 FXXLW 5
      |  |  |
Db      2 FSDLW 6

RESULT 5
US-09-903-412-36
; Sequence 36, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The sequence of the FG loop of ubiquitin-binding
; OTHER INFORMATION: monobody clone 213.
US-09-903-412-36

Query Match      87.0%; Score 20; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
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Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5
|
Db 1 FADLM 5

RESULT 6

US-09-096-749A-36
; Sequence 36, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1

TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-09-096-749A-36

Query Match 87.0%; Score 20; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5
|
Db 1 FADLM 5

RESULT 7

US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Patent No. US2002011947A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-252

Query Match 87.0%; Score 20; DB 8; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLM 5
|
Db 1 FSHLM 5

RESULT 8

US-09-884-456-8
; Sequence 8, Application US/09884456
; Publication No. US20030027317A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Oul-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Hepatitis C virus protease
; FILE REFERENCE: 223002010005
; CURRENT APPLICATION NUMBER: US/09/884,456
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/253,230
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 08/709,177
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: 08/440,548
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/350,884
; PRIOR FILING DATE: 1994-12-06
; PRIOR APPLICATION NUMBER: 07/680,296
; PRIOR FILING DATE: 1991-04-04
; PRIOR APPLICATION NUMBER: 07/505,433
; PRIOR FILING DATE: 1990-04-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: West Nile Fever virus
; FEATURE:
; OTHER INFORMATION: West Nile Fever virus protease
US-09-884-456-8

Query Match      87.0%; Score 20; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 1 FHTLW 5

RESULT 9
US-09-884-456-11
; Sequence 11, Application US/09884456
; Publication No. US20030027317A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Oui-Lim
; TITLE OF INVENTION: Hepatitis C virus protease
; FILE REFERENCE: 223002010005
; CURRENT APPLICATION NUMBER: US/09/884,456
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/253,230
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 08/709,177
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: 08/440,548
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/350,884
; PRIOR FILING DATE: 1994-12-06
; PRIOR APPLICATION NUMBER: 07/680,296
; PRIOR FILING DATE: 1991-04-04
; PRIOR APPLICATION NUMBER: 07/505,433
; PRIOR FILING DATE: 1990-04-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murray Valley virus
; FEATURE:
; OTHER INFORMATION: Murray Valley virus protease
US-09-884-456-11

Query Match      87.0%; Score 20; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 1 FHTLW 5

RESULT 10
US-09-884-456-14
; Sequence 14, Application US/09884456
; Publication No. US20030027317A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Oui-Lim
; TITLE OF INVENTION: Hepatitis C virus protease
; FILE REFERENCE: 223002010005
; CURRENT APPLICATION NUMBER: US/09/884,456
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/253,230

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; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 08/709,177
; PRIOR FILING DATE: 1996-09-06
; PRIOR APPLICATION NUMBER: 08/440,548
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/350,884
; PRIOR FILING DATE: 1994-12-06
; PRIOR APPLICATION NUMBER: 07/680,296
; PRIOR FILING DATE: 1991-04-04
; PRIOR APPLICATION NUMBER: 07/505,433
; PRIOR FILING DATE: 1990-04-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Kunjin virus
; FEATURE:
; OTHER INFORMATION: Kunjin virus protease
US-09-884-456-14

Query Match      87.0%; Score 20; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 1 FHTLW 5

RESULT 11
US-09-214-371-37
; Sequence 37, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickseley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac=Cys (Acrid)
; NAME/KEY: VARIANT
; LOCATION: (9)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-37

Query Match      87.0%; Score 20; DB 10; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 4 FSDLW 8

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RESULT 12
 US-09-214-371-38
 ; Sequence 38, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picksley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal
 ; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 ; FILE REFERENCE: 4-20937/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 38
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)
 ; OTHER INFORMATION: x = Ac-Cys
 ; NAME/KEY: VARIANT
 ; LOCATION: (9)
 ; OTHER INFORMATION: X = Pro-NH2
 US-09-214-371-38

Query Match 87.0%; Score 20; DB 10; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.2e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 Db 4 FSDLW 8

RESULT 13
 US-09-214-371-35
 ; Sequence 35, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picksley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal
 ; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 ; FILE REFERENCE: 4-20937/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide
 ; NAME/KEY: VARIANT

; LOCATION: (1)
 ; OTHER INFORMATION: x = Ac-Cys (Acrid)
 ; NAME/KEY: VARIANT
 ; LOCATION: (10)
 ; OTHER INFORMATION: x = Pro-NH2
 US-09-214-371-35

Query Match 87.0%; Score 20; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 Db 5 FSDLW 9

RESULT 14
 US-09-214-371-36
 ; Sequence 36, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picksley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal
 ; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 ; FILE REFERENCE: 4-20937/A/PCT
 ; CURRENT APPLICATION NUMBER: US/09/214,371B
 ; CURRENT FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: PCT/EP97/03549
 ; PRIOR FILING DATE: 1997-07-04
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 36
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:peptide
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)
 ; OTHER INFORMATION: x = Ac-Cys
 ; NAME/KEY: VARIANT
 ; LOCATION: (10)
 ; OTHER INFORMATION: x = Pro-NH2
 US-09-214-371-36

Query Match 87.0%; Score 20; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 Db 5 FSDLW 9

RESULT 15
 US-09-214-371-17
 ; Sequence 17, Application US/09214371B
 ; Patent No. US20010018511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picksley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal

; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17

Query Match 87.0%; Score 20; DB 10; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
Db 4 FSDLW 8

Search completed: February 12, 2003, 11:25:07
Job time : 4.33333 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:13:52 ; Search time 99.375 Seconds
(without alignments)
32.439 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 2260083

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:

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3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	91.3	11	6	US-08-277-660-16
2	21	91.3	15	23	US-09-936-956-10
3	20	87.0	5	1	PCT-US99-02405-11
4	20	87.0	5	1	PCT-US99-26277-114
5	20	87.0	5	20	US-09-601-558-11
6	20	87.0	5	22	US-09-831-047B-114

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7 20 87.0 5 22 US-09-831-047C-114 Sequence 114, App
8 20 87.0 5 22 US-09-894-594-11 Sequence 11, App
9 20 87.0 6 1 PCT-US99-25044-130 Sequence 130, App
10 20 87.0 6 6 US-08-277-660-2 Sequence 2, Appli
11 20 87.0 6 6 US-08-277-660-3 Sequence 3, Appli
12 20 87.0 6 16 US-09-214-371-83 Sequence 83, Appl
13 20 87.0 6 18 US-09-428-082-130 Sequence 130, App
14 20 87.0 6 18 US-09-428-082B-130 Sequence 130, App
15 20 87.0 6 19 US-09-563-286B-130 Sequence 130, App
16 20 87.0 6 19 US-09-563-286C-130 Sequence 130, App
17 20 87.0 6 21 US-09-732-384-4 Sequence 4, Appli
18 20 87.0 6 21 US-09-732-384-5 Sequence 5, Appli
19 20 87.0 6 25 US-10-155-059-1 Sequence 1, Appli
20 20 87.0 7 6 US-08-277-660-27 Sequence 27, Appl
21 20 87.0 7 14 US-09-096-749A-36 Sequence 36, Appl
22 20 87.0 7 20 US-09-637-614-36 Sequence 24, Appl
23 20 87.0 7 21 US-09-701-080A-24 Sequence 24, Appl
24 20 87.0 7 23 US-09-903-412-36 Sequence 36, Appl
25 20 87.0 7 25 US-10-165-155-36 Sequence 36, Appl
26 20 87.0 7 25 US-10-190-162-36 Sequence 36, Appl
27 20 87.0 8 1 PCT-US02-09105-304 Sequence 304, App
28 20 87.0 8 1 PCT-US02-09135-206 Sequence 206, App
29 20 87.0 8 1 PCT-US02-09188-604 Sequence 604, App
30 20 87.0 8 1 PCT-US02-09257-393 Sequence 393, App
31 20 87.0 8 1 PCT-US02-09370-621 Sequence 621, App
32 20 87.0 8 1 PCT-US02-09922-382 Sequence 382, App
33 20 87.0 8 7 US-08-344-185B-123 Sequence 123, App
34 20 87.0 8 7 US-08-344-185C-123 Sequence 123, App
35 20 87.0 8 8 US-08-424-550A-252 Sequence 252, App
36 20 87.0 8 8 US-08-424-550B-252 Sequence 252, App
37 20 87.0 8 8 US-08-467-344A-252 Sequence 252, App
38 20 87.0 8 8 US-08-486-749-252 Sequence 252, App
39 20 87.0 8 8 US-08-488-445A-252 Sequence 252, App
40 20 87.0 8 8 US-08-488-446-252 Sequence 252, App
41 20 87.0 8 18 US-09-458-297-203 Sequence 203, App
42 20 87.0 8 18 US-09-458-297-345 Sequence 345, App
43 20 87.0 8 18 US-09-458-297-475 Sequence 475, App
44 20 87.0 8 18 US-09-458-297-690 Sequence 690, App
45 20 87.0 8 18 US-09-458-297-902 Sequence 902, App

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ALIGNMENTS

RESULT 1
US-08-277-660-16
; Sequence 16, Application US/08277660
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-277-660-16

Query Match 91.3%; Score 21; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
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 Db 5 FSALW 9

RESULT 2

US-09-936-956-10
 ; Sequence 10, Application US/09936956
 ; GENERAL INFORMATION:
 ; APPLICANT: Kudos Pharmaceuticals Limited
 ; APPLICANT: Jackson, Stephen P
 ; APPLICANT: Durocher, Daniel
 ; TITLE OF INVENTION: Screening Methods Based on FHA Domains
 ; FILE REFERENCE: MEWE014
 ; CURRENT APPLICATION NUMBER: US/09/936,956
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: GB 9906432.1
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: GB 9915075.7
 ; PRIOR FILING DATE: 1999-06-28
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthesised
 ; NAME/KEY: MOD_RES
 ; LOCATION: (8)
 ; OTHER INFORMATION: PHOSPHORYLATION
 ; US-09-936-956-10

Query Match 91.3%; Score 21; DB 23; Length 15;
 Best Local Similarity 60.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
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 Db 9 FSALW 13

RESULT 3

PCT-US99-02405-11
 ; Sequence 11, Application PC/TUS9902405
 ; GENERAL INFORMATION:
 ; APPLICANT: Trustees of the University of Pennsylvania
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
 ; FILE REFERENCE: UPN3544
 ; CURRENT APPLICATION NUMBER: PCT/US99/02405
 ; CURRENT FILING DATE: 1999-02-04
 ; EARLIER APPLICATION NUMBER: 60/073,690
 ; PRIOR FILING DATE: 1998-02-04
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 11
 ; LENGTH: 5

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
 ; PCT-US99-02405-11

Query Match 87.0%; Score 20; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 4.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | |
 Db 1 FSLW 5

RESULT 4

PCT-US99-26277-114
 ; Sequence 114, Application PC/TUS9926277
 ; GENERAL INFORMATION:
 ; APPLICANT: The Wistar Institute of Anatomy and Biology
 ; APPLICANT: The Trustees of the University of Pennsylvania
 ; APPLICANT: Blaszczyk-Thurin, Magdalena
 ; APPLICANT: Keiber-Emmons, Thomas
 ; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
 ; FILE REFERENCE: WST93PCT
 ; CURRENT APPLICATION NUMBER: PCT/US99/26277
 ; CURRENT FILING DATE: 1999-11-05
 ; EARLIER APPLICATION NUMBER: 60/107,478
 ; EARLIER FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 114
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: peptido-mimetic of a Lewis antigen
 ; PCT-US99-26277-114

Query Match 87.0%; Score 20; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 4.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | |
 Db 1 FSLW 5

RESULT 5

US-09-601-558-11
 ; Sequence 11, Application US/09601558
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieber-Emmons, Thomas
 ; APPLICANT: The Trustees of the University of Pennsylvania
 ; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens
 ; FILE REFERENCE: UPN3567
 ; CURRENT APPLICATION NUMBER: US/09/601,558
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: PCT/US99/02405
 ; PRIOR FILING DATE: 1999-02-04
 ; PRIOR APPLICATION NUMBER: 60/073,690
 ; PRIOR FILING DATE: 1998-02-04
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
 ; US-09-601-558-11

Query Match 87.0%; Score 20; DB 20; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
DB 1 FSLWL 5

RESULT 6
US-09-831-047B-114
; Sequence 114, Application US/09831047B
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebert-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047B
; CURRENT FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: peptido-mimetic of a Lewis antigen

US-09-831-047B-114

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
DB 1 FSLWL 5

RESULT 7
US-09-831-047C-114
; Sequence 114, Application US/09831047C
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Blaszczyk-Thurin, Magdalena
; APPLICANT: Kiebert-Emmons, Thomas
; TITLE OF INVENTION: Compositions and Methods For Treatment of Cancer
; FILE REFERENCE: WST93AUSA
; CURRENT APPLICATION NUMBER: US/09/831,047C
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/107,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 5
; TYPE: PRT
; ORGANISM: peptido-mimetic of a Lewis antigen

US-09-831-047C-114

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
DB 1 FSLWL 5

Query Match 87.0%; Score 20; DB 20; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
US-09-894-594-11
; Sequence 11, Application US/09894594
; GENERAL INFORMATION:
; APPLICANT: Kiebert-Emmons, Thomas
; APPLICANT: Weiner, David B.
; APPLICANT: Monzavi-Karbassi, Behjatollah
; TITLE OF INVENTION: Peptide Mimotopes of Carbohydrate Antigens and DNA Molecules Encoded by Peptide Mimotopes
; TITLE OF INVENTION: Same
; FILE REFERENCE: UPN-3984
; CURRENT APPLICATION NUMBER: US/09/894,594
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: PCT/US99/02405
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,690
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: 60/214,517
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Novel Sequence

US-09-894-594-11

Query Match 87.0%; Score 20; DB 22; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
DB 1 FSLWL 5

RESULT 9
PCT-US99-25044-130
; Sequence 130, Application PC/TUS9925044
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: REIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: PCT/US99/25044
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MDM/HDM
; OTHER INFORMATION: ANTAGONIST PEPTIDE

PCT-US99-25044-130

Query Match 87.0%; Score 20; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
| |
DB 2 FSLWL 6

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RESULT 10
US-08-277-660-2
; Sequence 2, Application US/08277660
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHID
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660-2

Query Match 87.0%; Score 20; DB 6; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 11
US-08-277-660-3
; Sequence 3, Application US/08277660
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHID
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660-3

Query Match 87.0%; Score 20; DB 6; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 12
US-09-214-371-83
; Sequence 83, Application US/09214371B
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide, amin
; OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371-83

Query Match 87.0%; Score 20; DB 16; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 13
US-09-428-082-130
; Sequence 130, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH

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; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MDM/HDM
; OTHER INFORMATION: ANTAGONIST PEPTIDE
US-09-428-082-130

Query Match 87.0%; Score 20; DB 18; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 2 FSDLW 6

RESULT 14
US-09-428-082B-130
; Sequence 130, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-09-428-082B-130

Query Match 87.0%; Score 20; DB 18; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 2 FSDLW 6

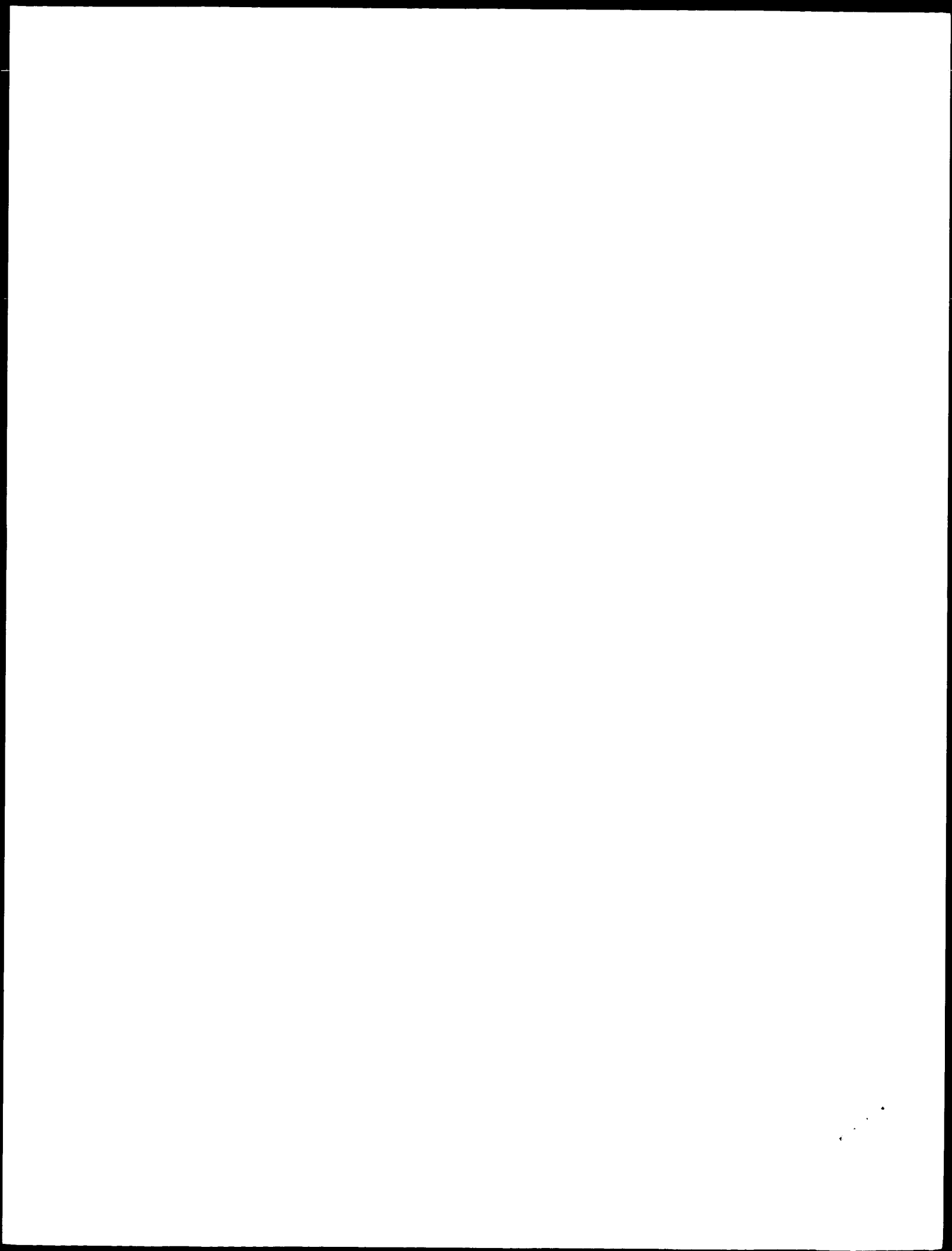
RESULT 15
US-09-563-286B-130
; Sequence 130, Application US/09563286B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/09/563,286B

; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1151
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mdm/hdm antagonist peptide
US-09-563-286B-130

Query Match 87.0%; Score 20; DB 19; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 2 FSDLW 6

Search completed: February 12, 2003, 11:24:04
Job time : 100.375 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 12, 2003, 11:14:12 ; Search time 7.08333 Seconds
(without alignments)
59.144 Million cell updates/sec

Title: US-09-403-440A-1

Perfect score: 23

Sequence: 1 FXXLW 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425801 seqs, 83787487 residues

Total number of hits satisfying chosen parameters: 159213

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New: *

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- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.psp.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.psp.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.psp.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.psp.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.psp.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	87.0	7	5	US-09-701-080C-12
2	20	87.0	7	6	US-10-174-717A-36
3	20	87.0	11	5	US-09-189-702A-286
4	20	87.0	13	5	US-09-701-080C-22
5	20	87.0	13	5	US-09-701-080C-27
6	20	87.0	15	6	US-10-211-088-141
7	20	87.0	19	7	US-60-438-805-9
8	20	87.0	20	1	PCT-US02-34021-343
9	20	87.0	22	6	US-10-203-138A-12722
10	19	82.6	5	5	US-09-281-717A-3
11	19	82.6	12	6	US-10-225-567A-2041
12	19	82.6	14	6	US-10-225-567A-2196
13	19	82.6	15	6	US-10-225-567A-1920
14	19	82.6	18	6	US-10-283-599-199
15	19	82.6	20	6	US-10-319-786-54
16	19	82.6	21	6	US-10-203-138A-12994
17	19	82.6	22	6	US-10-283-599-15
18	19	82.6	22	6	US-10-283-599-139
19	19	82.6	22	6	US-10-283-599-149
20	19	82.6	22	6	US-10-283-599-155
21	18	78.3	8	6	US-10-258-144-37
22	18	78.3	8	6	US-10-258-147-8
23	18	78.3	8	6	US-10-171-734-4
24	18	78.3	8	6	US-10-053-498B-144
25	18	78.3	10	5	US-09-863-054-27
26	18	78.3	10	6	US-10-099-056-2094

ALIGNMENTS

RESULT 1

US-09-701-080C-12

; Sequence 12, Application US/09701080C

; GENERAL INFORMATION:

; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY

; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F

; FILE REFERENCE: N73477C GCW

; CURRENT APPLICATION NUMBER: US/09/701,080C

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: GB 9811303.8

; PRIOR FILING DATE: 1998-05-26

; PRIOR APPLICATION NUMBER: GB 9900157.0

; PRIOR FILING DATE: 1999-01-05

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: derived from p53

US-09-701-080C-12

Query Match

Best Local Similarity 87.0%; Score 20; DB 5; Length 7;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

Db 1 FSDLW 5

RESULT 2

US-10-174-717A-36

; Sequence 36, Application US/10174717A

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; NUMBER OF SEQUENCES: 118

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.

; STREET: 121 South Eighth Street, St. 1600

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

;

;

; OPERATING SYSTEM: WINDOWS
 ; SOFTWARE: FastSeq Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/174,717A
 ; FILING DATE: 18-Jun-2002
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/096,749
 ; FILING DATE: June 12, 1998
 ; APPLICATION NUMBER: 60/049,410
 ; FILING DATE: June 12, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ann S. Vikenins
 ; REGISTRATION NUMBER: 37,748
 ; REFERENCE/DOCKET NUMBER: 109.034US4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (612) 373-6900
 ; TELEFAX: (612) 339-3061
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 ; US-10-174-717A-36

Query Match 87.0%; Score 20; DB 6; Length 7;
 Best Local Similarity 60.0%; Pred. No. 3.5e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | | |
 Db 1 FADLW 5

RESULT 3
 US-09-189-702A-286
 ; Sequence 286, Application US/09189702A
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Kast, W. Martin
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Epimmune, Inc.
 ; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
 ; FILE REFERENCE: 39963-20019.20
 ; CURRENT APPLICATION NUMBER: US/09/189,702A
 ; CURRENT FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; NUMBER OF SEQ ID NOS: 380
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 286
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p53.14 peptide 34.0324
 ; US-09-189-702A-286

Query Match 87.0%; Score 20; DB 5; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | | |
 Db 6 FSDLW 10

RESULT 4
 US-09-701-080C-22
 ; Sequence 22, Application US/09701080C
 ; GENERAL INFORMATION:
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
 ; FILE REFERENCE: N73477C GCW
 ; CURRENT APPLICATION NUMBER: US/09/701,080C
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: GB 9811303.8
 ; PRIOR FILING DATE: 1998-05-26
 ; PRIOR APPLICATION NUMBER: GB 9900157.0
 ; PRIOR FILING DATE: 1999-01-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:derived from p53
 ; US-09-701-080C-22

Query Match 87.0%; Score 20; DB 5; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | | |
 Db 5 FSDLW 9

RESULT 5
 US-09-701-080C-27
 ; Sequence 27, Application US/09701080C
 ; GENERAL INFORMATION:
 ; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
 ; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
 ; FILE REFERENCE: N73477C GCW
 ; CURRENT APPLICATION NUMBER: US/09/701,080C
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: GB 9811303.8
 ; PRIOR FILING DATE: 1998-05-26
 ; PRIOR APPLICATION NUMBER: GB 9900157.0
 ; PRIOR FILING DATE: 1999-01-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:derived from p53
 ; US-09-701-080C-27

Query Match 87.0%; Score 20; DB 5; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | | |
 Db 5 FSDLW 9

RESULT 6
 US-10-211-088-141
 ; Sequence 141, Application US/10211088
 ; GENERAL INFORMATION:
 ; APPLICANT: Bright, Gary R.
 ; APPLICANT: Premkumar, D. David

; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-141

Query Match 87.0%; Score 20; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 8 FSDLW 12

RESULT 7
US-60-438-805-9
; Sequence 9, Application US/60438805
; GENERAL INFORMATION:
; APPLICANT: KODAREK, THOMAS
; TITLE OF INVENTION: MIXED ELEMENT CAPTURE AGENTS
; FILE REFERENCE: UTSD:935USPI
; CURRENT APPLICATION NUMBER: US/60/438,805
; CURRENT FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-60-438-805-9

Query Match 87.0%; Score 20; DB 7; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 7 FSDLW 11

RESULT 8
PCT-US02-34021-343
; Sequence 343, Application PC/TUS0234021
; GENERAL INFORMATION:
; APPLICANT: DGI Biotechnologies, Inc.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009PC
; CURRENT APPLICATION NUMBER: PCT/US02/34021
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 343
; LENGTH: 20
; TYPE: PRT

; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGI7-20M-4-G12
PCT-US02-34021-343

Query Match 87.0%; Score 20; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 16 FFSWLW 20

RESULT 9
US-10-203-138A-12722
; Sequence 12722, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 12722
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009946.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; FEATURE:
; OTHER INFORMATION: EST_HUMAN HIT: AW452898.1, EVALUE 5.00e-03
US-10-203-138A-12722

Query Match 87.0%; Score 20; DB 6; Length 22;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
| | |
Db 6 FSQLW 10

RESULT 10
US-09-281-717A-3
; Sequence 3, Application US/09281717A
; GENERAL INFORMATION:
; APPLICANT: Baxter, John
; APPLICANT: Darimont, Beatrice
; APPLICANT: Feng, Weijun

; APPLICANT: Fletterick, Robert
; APPLICANT: Kushner, Peter
; APPLICANT: West, Brian
; APPLICANT: Wagner, Richard
; APPLICANT: Yamamoto, Keith
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING NUCLEAR RECEPTOR
; TITLE OF INVENTION: COACTIVATOR BINDING
; FILE REFERENCE: 9811-008-999
; CURRENT APPLICATION NUMBER: US/09/281.717A
; CURRENT FILING DATE: 1999-03-30
; PRIOR FILING DATE: 1998-03-30
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: Variant
; LOCATION: (2)...(3)
; OTHER INFORMATION: Xaa is any amino acid
US-09-281-717A-3

Query Match 82.6%; Score 19; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.5e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FXXLW 5
|
Db 1 FXXLW 5

RESULT 11
US-10-225-567A-2041
; Sequence 2041, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2041

Query Match 82.6%; Score 19; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
|
Db 2 FLFLW 6

RESULT 12
US-10-225-567A-2196
; Sequence 2196, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2196
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2196

Query Match 82.6%; Score 19; DB 6; Length 14;
Best Local Similarity 60.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
|
Db 3 FLILW 7

RESULT 13
US-10-225-567A-1920
; Sequence 1920, Application US/10225567A
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1920
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1920

Query Match 82.6%; Score 19; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

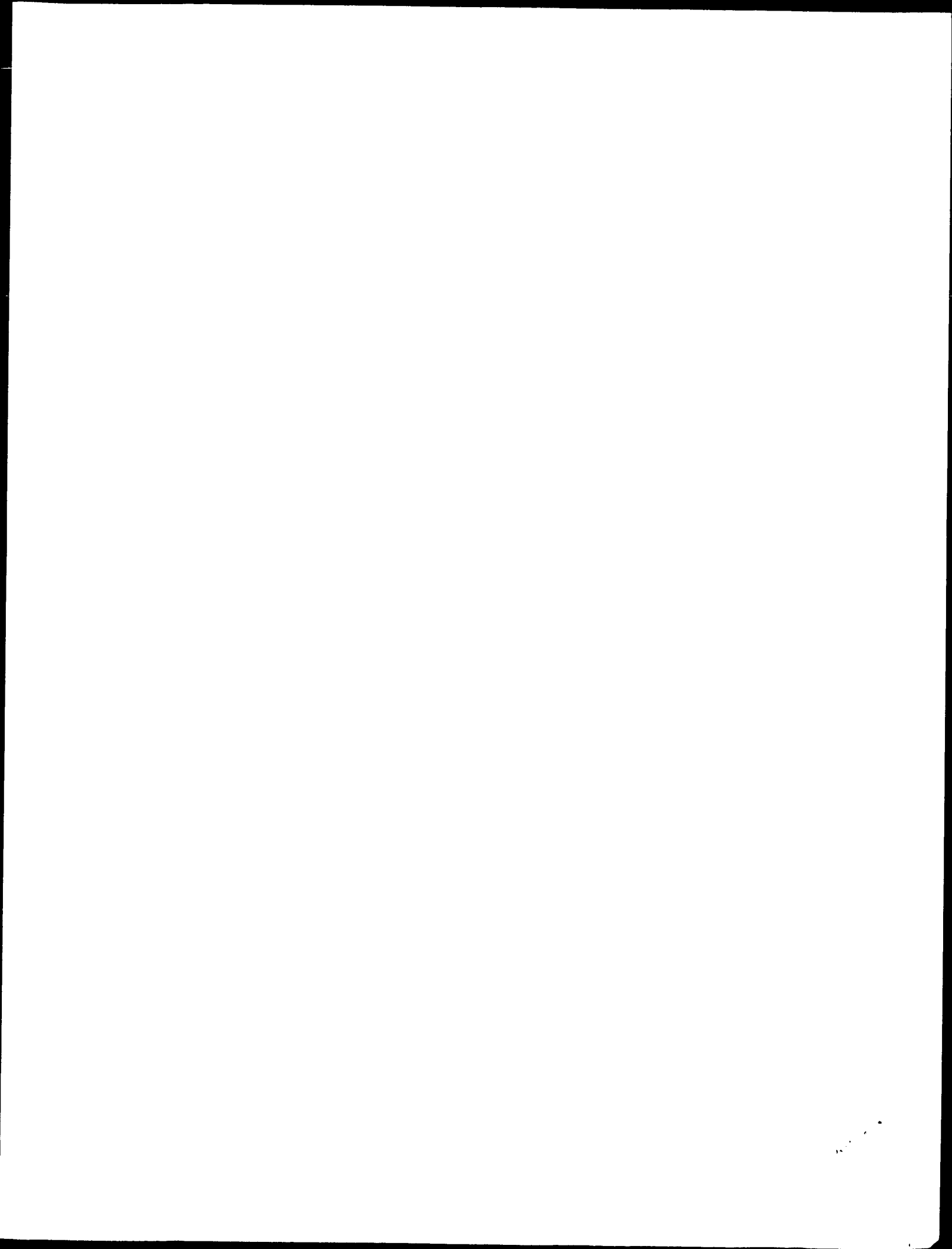
Qy 1 FXXLW 5
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Db 9 FRLWL 13

RESULT 14
US-10-283-599-199
; Sequence 199, Application US/10283599
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA

```

;
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,599
; FILING DATE: 29-OCT-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
;
; US-10-283-599-199
;
; Query Match 82.6%; Score 19; DB 6; Length 18;
; Best Local Similarity 60.0%; Pred. No. 9.4e+02;
; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 FXXLW 5
; DB 6 FRELW 10
;
; RESULT 15
; US-10-319-786-54
; Sequence 54, Application US/10319786
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G
; TITLE OF INVENTION: Biologically Active Peptides from
; Functional Domains of Bactericidal/Permeability-Increasing
; Protein and Uses Thereof
;
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/319,786
; FILING DATE: 13-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,344
; FILING DATE: 7-JUN-1995
; APPLICATION NUMBER: US 08/306,473
; FILING DATE: 15-SEP-1995
;
;
; APPLICATION NUMBER: US 08/209,762
; FILING DATE: 11-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 93,1133-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.7"
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
;
; US-10-319-786-54
;
; Query Match 82.6%; Score 19; DB 6; Length 20;
; Best Local Similarity 60.0%; Pred. No. 1e+03;
; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 FXXLW 5
; DB 8 FLKLW 12
;
; Search completed: February 12, 2003, 11:24:44
; Job time : 7.08333 secs

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QM protein - protein search, using sw model

Run on: February 12, 2003, 11:12:42 ; Search time 4.58333 Seconds
(without alignments)
32.098 Million cell updates/sec

Title: US-09-403-440A-1
Perfect score: 23
Sequence: 1 FXXLW 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 147762

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTRUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	91.3	11	1	US-08-277-660A-16
2	21	91.3	11	1	US-08-424-957-29
3	21	91.3	11	4	US-09-035-686-29
4	20	87.0	6	1	US-08-277-660A-2
5	20	87.0	6	1	US-08-277-660A-3
6	20	87.0	6	1	US-08-424-957-2
7	20	87.0	6	1	US-08-424-957-3
8	20	87.0	6	1	US-08-424-957-6
9	20	87.0	6	4	US-09-035-686-2
10	20	87.0	6	4	US-09-035-686-3
11	20	87.0	6	4	US-09-035-686-6
12	20	87.0	6	4	US-09-081-975-1
13	20	87.0	7	1	US-08-277-660A-27
14	20	87.0	7	1	US-08-424-957-15
15	20	87.0	7	1	US-08-424-957-19
16	20	87.0	7	4	US-09-035-686-15
17	20	87.0	7	4	US-09-035-686-19
18	20	87.0	7	4	US-09-638-202A-36
19	20	87.0	8	4	US-08-469-260A-252
20	20	87.0	9	1	US-08-350-884-8
21	20	87.0	9	1	US-08-350-884-11
22	20	87.0	9	1	US-08-350-884-14
23	20	87.0	9	1	US-08-709-173-8
24	20	87.0	9	1	US-08-709-173-11
25	20	87.0	9	1	US-08-709-173-14
26	20	87.0	9	1	US-08-638-911A-15
27	20	87.0	9	1	US-08-638-911A-18

Sequence 21, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-277-660A-16
; Sequence 16, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picklesley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660A-16

Query Match 91.3%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5

Db 5 FSALW 9

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RESULT 2
US-08-424-957-29
; Sequence 29, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-29

Query Match          91.3%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 5 FSALW 9

RESULT 3
US-09-035-686-29
; Sequence 29, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-29

Query Match          91.3%; Score 21; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
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Db 5 FSALW 9

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-29

Query Match          91.3%; Score 21; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
   |  |  |
Db 5 FSALW 9

RESULT 4
US-08-277-660A-2
; Sequence 2, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Pickseley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:

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SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-277-660A-2

Query Match 87.0%; Score 20; DB 1; Length 6;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
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 Db 2 FSDLW 6

RESULT 5
 US-08-277-660A-3
 ; Sequence 3, Application US/08277660A
 ; Patent No. 5702908
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/277,660A
 ; FILING DATE: 20-JUL-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-60244/WH
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-277-660A-3

Query Match 87.0%; Score 20; DB 1; Length 6;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | |
 Db 2 FSLGW 6

RESULT 6
 US-08-424-957-2
 ; Sequence 2, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.

APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957
 ; FILING DATE: 19-APR-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WH
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-424-957-2

Query Match 87.0%; Score 20; DB 1; Length 6;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
 | |
 Db 2 FSDLW 6

RESULT 7
 US-08-424-957-3
 ; Sequence 3, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Picksley, Steven M.
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957
 ; FILING DATE: 19-APR-1995

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-3

Query Match      87.0%; Score 20; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSGLW 6

RESULT 8
US-08-424-957-6
; Sequence 6, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-6

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Query Match      87.0%; Score 20; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSGLW 6

RESULT 9
US-09-035-686-2
; Sequence 2, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-2

Query Match      87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXLW 5
DB 2 FSGLW 6

RESULT 10
US-09-035-686-3
; Sequence 3, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.

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;;
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-3

Query Match 87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 11
US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Pickesley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-09-035-686-6

Query Match 87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSGLW 6

RESULT 12
US-09-081-975-1
; Sequence 1, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-975-1
Query Match      87.0%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 2 FSDLW 6

RESULT 13
US-08-277-660A-27
; Sequence 27, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/424,957
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-15
Query Match      87.0%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXLW 5
Db 1 FSDLW 5

RESULT 15
US-08-424-957-19
; Sequence 19, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-424-957-19
Query Match      87.0%; Score 20; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 FXXLW 5
Db 3 FSDLW 7

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Search completed: February 12, 2003, 11:15:59
Job time : 5.08333 secs

